Human mic Human mic Human mic Human mic Human mic Human mic

Newcastle S. cerevi M marinum S. aureus Human mic Human mic

Human sil

ASTHI pol Forward A Sequence 50 bp spa Human leu Human leu

Yeast acy Human spl Human sec

Rat splic Mouse spl Human col Human col

24 12.8 64.0 51 5 ABLO0484 25 12.8 64.0 58 3 AAA4622 26 12.8 64.0 74 4 AAR83273 27 12.6 63.0 20 7 AACCT3349 28 12.6 63.0 24 2 AAXC2618	12.6 63.0 25 8 12.6 63.0 25 8 12.6 63.0 25 8	12.6 63.0 25 8 12.6 63.0 25 8 12.6 63.0 25 8	12.6 63.0 25 8 12.6 63.0 25 8 12.6 63.0 25 8	12.6 63.0 27 2 12.6 63.0 27 3	12.6 63.0 27 7 12.6 63.0 34 2	12.6 63.0 50 6 12.6 63.0 50 6	12.6 63.0 50 6 12.6 63.0 55 6	12.6 63.0 60 3 12.6 63.0 60 6 12.6 63.0 63 3	12.6 63.0 65 6 12.6 63.0 65 6 12.6 63.0 74 7	12.6 63.0 74 7	12.4 62.0 20 6 12.4 62.0 25 8	12.4 62.0 25 8 12.4 62.0 25 8	12.4 62.0 25 8 12.4 62.0 25 8 12.4 62.0 47 3	62 12.4 62.0 50 6 63 12.4 62.0 51 5	64 12.4 62.0 60 6 65 12.4 62.0 60 6	12.4 62.0 65 6 12.2 61.0 20 2 12.2 61.0 21 4	12.2 61.0 23 6 12.2 61.0 23 6	12.2 61.0 23 6 12.2 61.0 23 7	12.2 61.0 23 7 12.2 61.0 23 7	12.2 61.0 23 7 12.2 61.0 23 7	12.2 61.0 23 7	12.2 61.0 23 7	12.2 61.0 23 7 12.2 61.0 23 7	12.2 61.0 23 7 12.2 61.0 23 7	12.2 61.0 23 8	12.2 61.0 23 8	12.2 61.0 23 9 12.2 61.0 24 3	12.2 61.0 25 2	12.2 61.0 25 8	12.2 61.0 25 8 12.2 61.0 26 2	94 12.2 61.0 32 7 95 12.2 61.0 33 2	12.2 61.0 33 2
5.1.6 Compugen Ltd.		without alignments) 74.659 Million cell	00			residues	mmeters: 3399856 c	0 0	80		O			0	rð	e of the result being pr score distribution.	IES	Description	Aci	Aaa61982 I	AAE88123	Ad168000 Ada13992	Ab199963 I Aaf77839 (	Aci17115	Aat89524 Bloom's	Abz29491 Cand Acd50544 HBV		Acido55 Human mic	AC101532 Huma ACh61845 DNA	Ach57384 Aas09822	Aaf8383 Human Chk	Aaz67540 Kuman map
GenCore version Copyright (c) 1993 - 2004	nuc.		itle: US erfect score: 20	e: I agraacarcrargrrygrr	Scoring table: IDENIITI NUC Gapop 10.0 , Gapext 1.0	Searched: 3373863 seqs, 2124099041 re	Total number of hits satisfying chosen parame	Minimum DB seq length: 0 Maximum DB seq length: 80	Post-processing: Minimum Match 0% Maxximum Match 100% Maxximum Afrot 150 giummaries	יייי הוארים הוויים ביויים ביוי	z'	<pre>3: geneseqn2000s:* 4: geneseqn2001as:* 5: qeneseqn2001bs:*</pre>	genesedn?	ċ	ordination imper of results	greater than or equal to the is derived by analysis of the	SUMMARIES	Result Query No. Score Match Length DB ID	14.4 72.0 25 8	13.8 69.0 20 3	13.8 69.0 33 4	13.8 69.0 33.4 13.8 69.0 43.3	7 13.6 68.0 24 6	13.4 67.0 25 8	11 13.2 66.0 24 2	13.2 66.0 65 6 12.8 64.0 17 7	14 12.8 64.0 17 7	12.8 64.0 25 8	12.8 64.0 25 8	12.8 64.0 25 8	21 12.8 6	12.8 64.0 43 5 12.8 64.0 47 3

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Oligonucl Human NR1 Human aux Primer fo

Human cyt CYP2D6 C1 Cytochrom Cytochrom CYP2D6 C1 Cytochrom Human CYP Serum and CFTR gene CFTR gene Human mic Human mic

5950 Human 3595 GM-CSF 3963 Human 1088 Human	1320 Human 1320 Human 7242 Human 7241 Human	1388 PCR pr 1388 PCR pr 4349 Human 6504 Human	2833 2873 2873 7367	22 Human 21 Human 22 Human 33 Rat sp	4055 HIV ga 5067 Inhibi 9957 Human 5982 Human 1018 Single	961 Single 964 Single 112 Single 991 Single 535 Human m	738334 748 748 748 748 748 748 748 748 748 74	237.0 numan 12815 Solanu 51102 Revers 51001 Revers 07616 RT-PCR 02624 Primer 12736 Mib qe	7164 Human 7165 Human 7334 Human 7058 Human 7759 Nucle 5677 PCR p 9293 Staph
AAT26950 AAT00595 AAH48963 ABZ44088 ABZ54030	ABL61320 AAD17242 AAD17241	ABC01388 ABZ04349 ABZ06504 ABZ06504	דעונמנ	AAT21822 ABN36821 ABN50252 ABN31593	Abau4055 Aba56067 Abc10957 Abh55982 Abc71018	AAC70961 AAC70964 AAC71012 AAC70991 AC183535	ALI/25/ ACI31661 ACI31661 ACI55181 ACI74139 ACI13584 ACI13296		AAA77164 AAA77165 ALZ7334 ABZ47058 ABL56759 AAV15677 AAV79293
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c 97 c 98 99 100 101	C 102 C 103 103	106 107 108 0 109		114 C 115 C 116		123 125 125 123 123			C 1443 C 1444 C 1455 146 147 C 149 C 150

ALIGNMENTS

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Human microarray DNA oligonucleotide SEQ ID NO 60525.
ACI60534 standard; DNA; 25 BP.
                           13-OCT-2003 (first entry)
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EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, cor family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid for the in situ hybridisation, in Southern, Northern or dottoprobes is useful in in situ hybridisation, in Southern, Northern or dottoprime extensions of any gene, in mapping the 5' termin of mutations of any gene, in mapping the 5' termin of mutations of any gene, in mapping the 5' termin of mutations of any gene, in mapping the 5' termin of mutations of any gene, in mapping the 5' termin of mutations of any gene, in mapping the 5' termin of mutations of any gene, in mappendic acid probes incorporated in the microarray. Note: The sequence containing segments of DNA that have been incorporated in the microarray. Note: The sequence of the mutations of any sequence of the microarray. Note: The sequence of the form USPPO at sequence of the microarray.
                                                                                                                                                                                                                                                                                                                                                                                                                              New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 60525; 9pp; English.
                                                                                                                                                              15-MAR-2002; 2002US-00098263.
                                                                                                                                                                                                             16-MAR-2001; 2001US-0276759P.
                                                                                                                                                                                                                                                                     (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-567953/53.
                                                    US2003104410-A1.
     Homo sapiens.
                                                                                                                                                                                                                                                                                                                          Mittmann MP;
                                                                                                         05-JUN-2003
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Sequence 25 BP; 7 A; 4 C; 5 G; 9 T; 0 U; 0 Other;

Gaps .. 0 72.0%; Score 14.4; DB 8; Length 25; 93.8%; Pred. No. 2.8e+03; Live 0; Mismatches 1; Indels Query Match
Best Local Similarity 93.8
Matches 15; Conservative

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1 AGTAACATCTATGTTT 16

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Human MEKK5 phosphorothioate antisense oligonucleotide, SEQ ID NO:34.
                                       AAA61982 standard; DNA; 20 BP
3 AGTAACATCGATGTTT 18
                                                                      (first entry)
                                                                      20-NOV-2000
                                                       AAA61982;
                        RESULT 2
                                AAA6198;
Db
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Human MEXK5; mitogen-activated protein kinase kinase 5; MAP/ERK kinase 5; ASK1; pro-apoptotic; MEK kinase 5; MAP/ERK kinase 1; ASK1; pro-apoptotic; apoptosis signal-regulating kinase 1; programmed cell death; serime/threonine kinase; MAP kinase cascade; JNK/SAPK module; Jun N-terminal kinase; kinase activated protein kinase; p38 module; SEK1; transcription factor modulation; expression inhibition; antisense;

Lakner M;

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Claim 3; Col 39; 35pp; English.
                                                                                                                                                                                                                1 AGTAACATCTATGTTG 17
                                                                                                                                                                                                                      2 AGTAACATCTGTCTTTG 18
                                                                                                                                                                                                                                            AAA40172 standard; DNA; 33 BP
                                                                                                                                                                                                        15; Conservative
                                                                                                                                                                                wound healing disorders
                                                (ISIS-) ISIS PHARM INC
                                                        Cowsert LM,
                                                                WPI; 2000-464034/40.
                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                            01-NOV-2000
                                        23-JUL-1999;
                                23-JUL-1999;
        Homo sapiens
                US6080546-A
                        27-JUN-2000.
                                                        Monia BP,
                                                                                                                                                                                                                                                     AAA40172;
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                                                                                                                                                                                                        Matches
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This invention describes a novel method for the detection of a mammalian infection by an acid-resistant microorganism (A) by treating a faecal sample with at least two different monoclonal antibodies (MAD) for their fragments or derivatives) or aptamers (collectively (I)) and detecting formation of a complex (C) between (I) and the corresponding antigen of formation of a complex (C) between (I) and the corresponding antigen of (A). The first and second (I) bind to epitopes of different antigens (Ag). These epitopes are present, after passage through the intestines, in at least some mammals, and have either: (i) their native structure; or (ii) a structure against which an antibody is produced by an animal ciffered or immunized with (A), or its extract, lysate, derived protein or fragment, or with a synthetic peptide. Practically all mammals display or least one of the specified epitopes. The method is used to detect infection by acid-fast bacteria, particularly of the genera Helicobacter, Mycobacterium and Campylobacter, specifically H. Pylori, H. hepaticus, M. therapeutically. The method is direct and non-invasive, and provides an inexpensive and easily standardizable diagnosis, despite possible degradation of antigens during passage through the intestines. This sequence encodes a fragment of a H. Pylori beta-urease-binding antibody illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting infection by acid-fast microbes for diagnosis of Helicobacter pylori, comprises reacting a fecal sample with two binding reagents for antigens that survive intestinal passage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.0%; Score 13.8; DB 3; Length 33; 88.2%; Pred. No. 5.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33 BP; 10 A; 6 C; 7 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                    Friedrichs U, Heppner P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 29; Page 23; 84pp; German.
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                                                                                                                                                      98EP-00120517.
98EP-00120687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Conservative
                                                                                                                                                                                                                                                                                         Cullmann G,
                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-365747/31.
P-PSDB; AAB10016.
                                                                                                                                                                                                                                     (CONN-) CONNEX GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
WO200026671-A1
                                                                                                                                                                                    06-NOV-1998;
                                                                                                     29-OCT-1999;
                                                                                                                                                         29-OCT-1998;
                                                 11-MAY-2000.
                                                                                                                                                                                                                                                                                    Reiter C,
Ringeis A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression. The antisense oligonucleotides were designed to target carpersation. The antisense oligonucleotides were designed to target carpersations of the human MEKKS RNA, and were analysed for their effect on MEKKS mRNA levels by quantitative real-time PCR. MEKKS (also known as mitogen-activated protein kinase kinase 5, MEK kinase 5, apoptosis signal-regulating kinase 1, and ASK1) is a dual-specific serine/threonine kinase which mediates cellular responses to mitogenic stimuli by activating both the JNK/SAPK (JUN N-terminal kinase/stress-activated protein kinase) and p38 modules of MAP carminal kinase/stress-activated protein kinase) and p38 modules of MAP capulation of apoptosis (programmed cell death) by interacting with other spotesis in this cascade and by phosphorylating downstream targets such as MKK3 and SEKI. MEKK5 as participates in another apoptosis-related signalling cascade involving the modulation of transcription factors. Activation and dimerisation of MEKK5 is induced by tumour necrosis factor-alpha (TNP-alpha), these processes being mediated by reactive oxygen capetions are useful for diagnosis, prevention and treatment of conditions associated with MEKK5 expression, such as inflammation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense compounds useful for treating or preventing infection, inflammation or tumor formation by inhibiting expression of human MEKKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences AAA61956-A61995 represent phosphorothioate antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.0%; Score 13.8; DB 3; Length 20; 88.2%; Pred. No. 5.3e+03; ive 0; Mismatches 2; Indels
inflammation; wound healing disorder; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 4 A; 4 C; 4 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                      Gaarde W;
                                                                                                                                                                                                             99US-00359757
                                                                                                                                                                                                                                                                 99US-00359757
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0

Gaps

; 0

Indels

Catalase; beta-urease; antibody; antigen; detection; infection; epitope; acid-resistant microorganism; complementarity determining region; CDR; feces; heavy chain; light chain; ds.

WO200127612-A2

Unidentified.

Acid-resistant microorganism; detection; faecal; intestine; infection; monoclonal antibody; light chain; complementarity determining region; CDR; beta-urease; ss.

Unidentified

H. pylori beta-urease-binding antibody light chain CDR1 DNA #2.

H. pylori beta-urease derived antibody light chain CDR1 DNA #2.

Haindl E;

Mueller H,

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This invention describes a novel method for detecting, in a mammal, infection by an acid-resistant microorganism (A) which comprises reacting a fecal sample with: (i) a receptor (R) such that a complex is formed with an antigen (Ag) of (A), or (ii) two different R so that a three-part complex is formed with Ag, and the formation of a complex detected. R are specific for an Ag which, after passage through the intestines, at least in some mammals, retains a native (or corresponding) structure against on its extracts, lysates or derived proteins (or fragments) or synthetic peptides). The products of the invention have antibacterial activity. The method is used to diagnose infection by Helicobacter, Campylobacter or Mycobacterium, particularly H, pylori (most preferred), H, hepatica, C. jejuni and M. tuberculosis, and also to monitor the progress of treatment. Receptors, particularly antibodies, directed progress of treatment. Receptors, particularly antibodies, directed against Ag can be used therapeutically for treatment of infections. The method requires only one R to provide a reasonably secure diagnosis (although use of two R improves sensitivity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Geranylgeranyl diphosphate synthase; GGPP synthase; yew; cytostatic;
anticancer; Taxus; diterpene; paclitaxel; identification; plant;
Taxomyces andreanae; Penicillium raistrickii; microorganism; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CDR) from an antibody generated against a Helicobacter pylori antigen (catalase or beta-urease) which is used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inexpensive and more easily standardized. Also it is direct, non-
invasive, suitable for automation and may indicate the stage of an
infection. This sequence encodes a complementarity determining region
                                                                                                                                                                                                                                                                                               Detecting infections by acid-resistant microorganisms, particularly diagnosing Helicobacter pylori, comprises an immunoassay on a fecal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.0%; Score 13.8; DB 4; Length 33; 88.2%; Pred. No. 5.4e+03; ive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 33 BP; 10 A; 6 C; 7 G; 10 T; 0 U; 0 Other;
                                                                                                        (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
                                                                                                                                                           Cullmann G, Heppner P, Ringeis A,
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 26; Page 18; 89pp; German.
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                         31-MAR-2000; 2000EP-00107028.
10-MAY-2000; 2000EP-00110110.
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les 15, Conservative
                                                                                                                                                                                                                WPI; 2001-282087/29.
                                                                                                                                                                                                                                               P-PSDB; AAB86064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid-resistant microorganism (A), in a mammal, using immercion by an acid-resistant microorganism (A), in a mammal, using immunochromatography. The method is used to diagnose infection by an acid resistant microorganism (A), in a mammal, such as Helicobacter. Campylobacter or Mycobacterium, particularly H. pylori (most preferred), H. hepatica, C. jejuni and M. tuberculosis. The method is rapid, simple, inexpensive and non-invasive, and may indicate the stage of infection. A test strip used in the method may include a filter to eliminate particles present in the sample and only a single receptor provides a reasonably secure diagnosis, with specificity and selectivity improved by detecting several epitopes (of catalase) or different antigens (catalase and betaurease). The method can be automated. This sequence encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting infections by acid-resistant microorganisms, particularly for diagnosing Helicobacter pylori, comprises immunochromatographic detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heavy chain; light chain; catalase; beta-urease; detection; CDR; antigen; infection; acid-resistant microorganism; fecal; antibody; diagnosis; antibacterial; complementarity determining region; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complementarity determining region (CDR) from an antibody raised against the H. pylori catalase or beta-urease antigen which is used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel method for detecting infection by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                         Schwartz G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.0%; Score 13.8; DB 4; Length 33; 88.2%; Pred. No. 5.4e+03; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                      Lakner M, Truee A, Dehnert S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33 BP; 10 A; 6 C; 7 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                             (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 30; Page 28; 90pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF88066 standard; DNA; 33 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 AACAICIAIGITIGGIT 20
                                                                                                                            12-OCT-1999; 99EP-00120351.
16-MAR-2000; 2000EP-00105992.
31-MAR-2000; 2000EP-00107028.
10-MAY-2000; 2000EP-00110110.
                                                                         12-OCT-2000; 2000WO-EP010057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99EP-00120351.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 AACATTAATGTTTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Conservative
                                                                                                                                                                                                                                                                                                                      Reiter C, Cullmann G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of antigen in feces.
                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-282086/29.
P-PSDB; AAB86096.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200127613-A2.
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                      19-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUL-2001
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AAF88066;

AAF88066

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Query Match Matches

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Gaps

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The present sequence represents a PCR primer for a geranylgeranyl diphosphate (GGPP) synthase protein. GGPP synthase has cytostatic activity. A vector encoding GGPP synthase is useful in increasing GGPP synthase levels in a host cell preferably Taxus (Yew) cell and thereby facilitates production, isolation and purification of larger amounts of GGPP synthase in plants. GGPP synthase is useful in obtaining expression or enhanced expression of GGPP and other diterpens, such as paclitaxel, useful as anticancer drugs. Isolated nucleic acids encoding GGPP synthase or hybridising with GGPP synthase encoding nucleic acids are used for identifying genes encoding GGPP synthase from microorganisms such as
                                                                                                                                                                                                  Nucleic acid encoding geranylgeranyl diphosphate is useful for producing paclitaxel and other diterpenes that are useful as anticancer drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13.8; DB 3; Length 43; Pred. No. 5.5e+03; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 43 BP; 14 A; 6 C; 10 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Taxomyces andreanae and Penicillium raistrickii
                                                                            (UNIW ) UNIV WASHINGTON STATE RES FOUND.
                                                                                                                                                                                                                                                                Example 2; Col 41; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.0%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 88..
Loca 15; Conservative
                                                                                                                     Croteau RB, Hefner JL;
                                                                                                                                                           WPI; 2000-282526/24
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2 AAGATCTATGTTTGATT 18 4 AACATCTATGTTTGGTT à d

ABL99963 standard; DNA; 24 BP ABL99963; ABL99963/c RESULT 7 THE LANGE OF THE PARTY OF THE P

(first entry) 08-AUG-2002

HOMO 2-hydroxy acid dehydrogenase family protein 26.29 PCR primer 2.

Human; DNA dependent 2-hydroxy acid dehydrogenase protein; enzyme; cytostatic; virucidal; immunomodulatory; antiinflammatory; haemostatic; malignant tumour; human immunodeficiency virus; HIV; infection; malignant tumour; human immunodeficiency virus; HIV; immunological disease; gene therapy; PCR; primer; ss

Homo sapiens

WO200232950-A1

25-APR-2002

02-JUL-2001; 2001WO-CN001128

07-JUL-2000; 2000CN-00117047

(BIOW-) BIOWINDOW GENE DEV INC SHANGHAI

Mao Y, Xie Y;

WPI; 2002-340232/37.

Polypeptide-HOMO DNA-dependent 2-hydroxy acid dehydrogenase family protein 26.29 and encoding polynucleotide, used in diagnosis and treatment of e.g. malignant tumors, hemopathy, immunological diseases and phlogosis.

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The invention relates to HOMO DNA-dependent 2-hydroxy acid dehydrogenase family protein 26.29 with cytostatic, virucidal, immunomodulatory, antinfilammatory and haemostatic activity. The protein and encoding polynucleotide are used in diagnosis and treatment of malignant tumour, haemopathy, human immunodeficiency virus (HIV) infection, immunological diseases and various inflammations. The polynucleotide is useful in gene therapy. The present sequence is that of a HOMO DNA-dependent 2-hydroxy acid dehydrogenase family protein 26.29 PCR primer, useful in examples of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a method for producing 1,3-propanediol from a carbon source, comprising culturing a recombinant microorganism having glycerol dehydratase and/or 1,3-propanediol dehydrogenase from Clostridium butyricum (see AAB73300, AAB80887 and AAB80889). The method of the present invention is useful for the production of 1,3-propanediol, which is useful as a stabiliser for lipases, amylases and proteases in wash liquids, as a protective emollient in liquid detergents for hand and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Production of 1,3-propanediol comprises culturing a recombinant microorganism expressing coenzyme B12-independent glycerol dehydratase.
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dish washing, and as a monomer for producing polymers, especially polyesters, polyethers and polyurethanes. The present sequence is a promoter sequence, for glycerol dehydratase, which was used in the
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                                                                                                                                                                                                                                                            Score 13.6; DB 6; Length 24;
Pred. No. 6.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycerol dehydratase, 1,3-propanediol; enzyme stabiliser; polymer production; promoter; enzyme; ss.
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                           Sequence 24 BP; 13 A; 2 C; 2 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 28 BP; 16 A; 2 C; 2 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INST NAT RECH AGRONOMIQUE.
NAT SCI APPLIQUEES TOULOUSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycerol dehydratase promoter sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Soucaille P;
              Example 2; Page 13; 37pp; Chinese.
                                                                                                                                                                                                                                                                                                                                   1 AGTAACAICTAIGITIGGIT 20
                                                                                                                                                                                                                                                                                                                                                              22 AGTAACTTCTATATTTTGAT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 18; Page 37; 69pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CENT NAT RECH SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
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                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
AAF77839/c
ID AAF77839 standard; DNA; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-247136/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention
                                                                                                                                                                                           the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF77839;
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Best Local Similarity
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Also disclosed is a method of gene expression analysis. The array is used in manitoring gene expression levels by hybridisation to a DNA library, or naulysis of geneit variation or in hybridisation to a DNA library, or factoring gene expression levels by hybridisation to a DNA library, of at least one target sequence. The method of analysis comprises compounds. The nucleic acid probes are specifically designed for analysis of probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring can eamily members of a gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gen and a cross-species comparison. Bach of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes in ni situ hybridisation, in Southern, Northern or dotblot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termin of mRNA molecules by primer extensions or in screening only and primer extensions or independent of many hyper hyperical many probes in screening only and proper many and a probes or subclones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.goc/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                                        .,
                        Score 13.6; DB 4; Length 28;
Pred. No. 6.7e+03;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Human microarray DNA oligonucleotide SEQ ID NO 17106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25 BP; 9 A; 5 C; 8 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 17106; 9pp; English.
                                                                                                                  1 AGTAACATCTATGTTTGGTT 20
                                                                                                                                                             26 AATAACATTTTTGTTTTT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-2002; 2002US-00098263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-2001; 2001US-0276759P.
                        68.0%;
80.0%;
                                                                                                                                                                                                                                                                               ACI17115 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cross-species comparison.
                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-567953/53.
              Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2003104410-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                            13-0CT-2003
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                                                                                                                                                                                                                                                                                                                             ACI17115;
                                                                                                                                                                                                                                                         ACI17115/c
                                                                                                                                                                                                                                 RESULT 9
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DB 8; Length 25;

67.0%; Score 13.4;

Query Match

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Suggenties Android-Tables in the manner of the suggesties which contains bidglefic polymorphic markers. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in a method for determining polymorphic forms in an individual. The invention further provides computer-readable storage medium for storing data for access by an application programme being executed on a data processing system. Such a method comprises a data structure stored in the computer-readable storage medium, the data structure including information records, each record comprising structure including information records, each record comprising information factors and methods can be used for analysing polymorphic sites in information should be used for analysing polymorphic sites in individuals for testing for the presence of a disease phenotype or in formation; paternity testing or genetic mapping of phenotypic traits. They can also be used for the production of transgenic animals. The nucleic acid segments can also be used in the manufacture of medicaments for the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid segments containing polymorphic sites - used for, e.g. detecting a disease phenotype, in forensics, paternity testing or genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphism; biallelic; paternity testing; forensic; genetic mapping; phenotypic typing; medicament; disease; marker; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences AAX06101-X06558 represent human DNA fragments which contain
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human biallelic polymorphic DNA fragment SGC34498.
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Pred. No. 8.3e+03;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berno A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment or prophylaxis of diseases
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                                                                                                                                                                                                                                                                                              AAX06450 standard; DNA; 31 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detecting a disease phenotype mapping of phenotypic traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US012930.
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Conservative
                                                                                                                                             16 carcrerrieerr 2
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                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                              14; Conservative
                                                                                      6 CATCTATGTTTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chee M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-080963/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09858529-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lipshutz RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                         AAX06450;
                                                                                                                                                                                                                                                                      AAX06450/c
                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
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WO200253728-A2
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                               11-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACD50544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACD50544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence that encodes an enzymatically active BLM protein. This is used in the Single-Strand Conformation Polymorphism (SSCP) Analysis of the BLM gene. SSCP analysis helps in identifying the mutants in the BLM gene. Bloom's syndrome is diagnosed by detecting 2 mutated BLM genes or the absence of a wild-type BLM gene in a subject. Delivery of a functional BLM gene to bone marrow cells is used to treat or prevent the onset of Bloom's syndrome. Identification of the BLM gene and its products should assist in the development of therapeutic and diagnostic agents for cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosing Bloom's syndrome, and carriers, by detecting mutant BLM genes - for gene therapy with nucleic acid encoding active BLM protein to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
                                                                                                                                                                cancer; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This forward primer is used in the PCR amplification of the BLM gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Candida gene related tetracyclin promoter PCR primer SEQ ID NO 3574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                             BLM; Bloom's syndrome; BS; mutant; probe; PCR primer; cancer; diagnosis; SSCP; Single-Strand Conformation Polymorphism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.0%; Score 13.2; DB 2; Length 24; 83.3%; Pred. No. 1e+04; ive 0; Mismatches 3; Indels
                                                                                                                              Bloom's syndrome active BLM gene SSCP forward primer C1-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24 BP; 7 A; 4 C; 5 G; 8 T; 0 U; 0 Other;

    for gene therapy with nucleic acid en
Bloom's syndrome and cancer in general.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 31; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               (NYBL-) NEW YORK BLOOD CENT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AGTAACATCTATGTTTGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23
                                                                                                                                                                                                                                                                                                                                                                                                                                  Groden J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABZ29491 standard; DNA; 65 BP
                                                                                                                                                                                                                                                                                                                                 96WO-US019046.
                                                                                                                                                                                                                                                                                                                                                                95US-00559303
                               AAT89524 standard; cDNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 AGTACCATCAATGATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  German J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-289051/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Candida albicans
                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                               WO9717979-A1
                                                                                                                                                                                                                                                                                                                               15-NOV-1996;
                                                                                               27-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                L5-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2003
                                                                                                                                                                                                                                                                                                22-MAY-1997
                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABZ29491;
                                                               AAT89524;
                                                                                                                                                                                                                                                                                                                                                                                                                                Ellis N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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RESULT 12

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The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by insertion of a promoter replacement fragment with a heterologous recombination, of a promoter replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells having both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modulates the compound catabolism biosynthetic, transporter, transcriptional, compound catabolism biosynthetic, transporter, transcriptional, compound is useful for identifying a compound having the activity. The method is useful for identifying a compound having the activity to inhibit growth or proliferation of cataborans cells and for treating infection by C. albicans. The present sequence is that of a PCR brine trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid molecule, Hepatitis C virus, HCV; Hepatitis B virus, HBV; RNA stability, RNA expression, RNA synthesis, antisense; enzymatic nucleic acid, hammerhead ribozyme; DNAzyme; inozyme; zinzzyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptemer; HBV reverse transcriptase; Enhancer I region; viral replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 76; SEQ ID NO 3574; 167pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13.2; DB 6; Length 65;
Pred. No. 1.1e+04;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 65 BP; 17 A; 12 C; 14 G; 22 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                          Ohlsen KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HBV hammerhead ribozyme substrate sequence #112.
                                                                                                                                                                                                                                                                                                                                                          Bussey H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                          Boone C,
                                                                                    29-DEC-2000; 2000US-0259128P.
                                                                                                                              20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
26-DEC-2001; 2001WO-US049486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 66.0%;
Best Local Similarity 83.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GTAACATCTATGTTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 GTAACATTCAAGTTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACD50544 standard; RNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                 (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                          Roemer T, Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-566694/60
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Nucleic acid molecule, Hepatitis C virus, HCV; Hepatitis B virus; HBV; RNA stability; RNA expression; RNA synthesis; antisense; enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptamer; HBV reverse transcriptase; Enhancer I region; viral replication; degenerative; disease state; HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;

substrate sequence #147.

HBV inozyme 24-SEP-2003

(first entry)

ACD51915;

virucide; antiinflammatory; substrate; ss.

Hepatitis B virus.

WO200281494-A1.

17-OCT-2002.

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The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes, include antisense care nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV C as oligonucleotides that specifically bind the Enhancer I region of HBV C Genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds and/or potential therapies directed against HBV, and compounds and/or potential therapies directed against HBV, and compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents a substrate for one of the HBV ribozyme, inozyme, inozyme, zinzyme, DNAzyme or amberzyme sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus
degenerative, disease state, HBV infection, HCV infection, cirrhosis, liver failure, hepatocellular carcinoma, hepatotropic, cytostatic, virucide, antiinflammatory, substrate, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.0%; Score 12.8; DB 7; Length 17; 50.0%; Pred. No. 1.6e+04; ive 6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mcswiggen J, Morrissey D, Pavco P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 BP; 4 A; 4 C; 3 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 138; 387pp; English.
                                                                                                                                                                                                          2001US-0296876P.
2001US-0296876P.
2001US-0335059P.
                                                                                                                                                              26-MAR-2002; 2002WO-US009187.
                                                                                                                                                                                             2001US-00817879.
                                                                                                                                                                                                                                                          05-DEC-2001; 2001US-0337055P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                          RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macejak D,
Roberts E;
                                                                                                                                                                                                                                                                                                                                      MCSWIGGEN J. MORRISSEY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-229207/22.
                                                                                                                                                                                                                                                                                                         BLATT L.
MACEJAK D.
                                                                                                                                                                                                                                                                                                                                                                     PAVCO P.
LEE P.
DRAPER K.
                                                                 Hepatitis B virus,
                                                                                                                                                                                                                                                                                                                                                                                                                        ROBERTS E.
                                                                                               WO200281494-A1.
                                                                                                                                                                                                                           08-JUN-2001;
                                                                                                                                                                                                                                             24-OCT-2001;
                                                                                                                                                                                                            08-JUN-2001;
                                                                                                                               17-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blatt L, I
Draper K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection.
                                                                                                                                                                                                                                                                                                        (BLAT/)
(MACE/)
                                                                                                                                                                                                                                                                                                                                                                     (PAVC/)
(LEEP/)
                                                                                                                                                                                                                                                                                          RIBO-)
                                                                                                                                                                                                                                                                                                                                      (MCSW/)
                                                                                                                                                                                                                                                                                                                                                                                                                      ROBE/)
                                                                                                                                                                                                                                                                                                                                                                                                       DRAP/)
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26-MAR-2001; 2001US-00817879. 08-JUN-2001; 2001US-00877478. 08-JUN-2001; 2001US-0296876P. 24-OCT-2001; 2001US-0335059P.

05-DEC-2001; 2001US-0337055P RIBOZYME PHARM INC

MACEJAK D. MCSWIGGEN J. MORRISSEY D.

(BLAT/) (MACE/) (MCSW/) (RIBO-)

(MORR/) | (PAVC/) | (LEEP/)

26-MAR-2002; 2002WO-US009187.

```
The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as harmerhead ribozymes, DNazymes, inczymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed are nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase and/or HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           that modulate the expression and/or replication of HCV. The compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular cardinoma. The present sequence represents a substrate for one of the HBV ribozyme, inozyme, G-cleaver, zinzyme, DNAzyme or amberzyme sequences disclosed in the present invention
                                                                                                           Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 BP; 5 A; 3 C; 3 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 152; 387pp; English.
WPI; 2003-229207/22
                                                                                                                                                                                                                                         infection.
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Gaps

; 0

16

1 AGTAACATCTATGTTT

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AGGAACCUCUAUGUUU 16

Score 12.8; DB 7; Length 17; Pred. No. 1.6e+04;

64.0%; 50.0%;

Query Match Best Local Similarity

ACD51915 standard; RNA; 17 BP.

RESULT 14 ACD51915

<u>а</u> Lee

Pavco P,

Mcswiggen J, Morrissey D,

Roberts E;

Draper K,

Blatt L, (DRAP/) (ROBE/)

Macejak D,

ROBERTS E. PAVCO P. LEE P. DRAPER K.

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13-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AGTAACATCTATGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cross-species comparison.
                                                                                       (AFFY-) AFFYMETRIX INC
                                                                                                                        WPI; 2003-567953/53.
                  US2003104410-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Homo sapiens.
                                                                                                        Mittmann MP;
                                  05-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACI01532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACI01532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
 ö
                                                                                                                                                                                                                                                                                                                                                                Duplex DNA (AAQ21864) (adapted from the L1 region of Human papilloma virus type 16) was used as a target to study the linear pre-amplification process. A probe set (QQ21865-8) was designed to hybridise to the target sequence for use in pre-amplification. The 3' end of probe 179.3 was haptenated with biotin-aminocaproyl NHS active ester. See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
 Gaps
                                                                                                                                                                                                                                                                                                               Target-dependent prodn. of templates for ligase chain reaction -
increases sensitivity and detection of target from non-target contg.
                                                                                                                                                   Templates; Human papilloma virus; ligase chain reaction; LCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 12.8; DB 2; Length 25;
Pred. No. 1.6e+04;
0; Mismatches 2; Indels
                                                                                                                                  Probe 179.3 DNA, to demonstrate controlled amplification.
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human microarray DNA oligonucleotide SEQ ID NO 60526.
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25 BP; 11 A; 6 C; 2 G; 6 T; 0 U; 0 Other;
 2;
 Mismatches
                                                                                                                                                                                                                                                                              Shimer GH;
                                                                                                                                                                                                                                                                                                                                                  Example 4; Page 7; 20pp; English.
 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВР
                                                                         867/c
AAQ21867 standard; DNA; 25 BP.
                                                                                                                                                                                                                           91EP-00114541.
                                                                                                                                                                                                                                           90US-00575177
                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 64.0%;
.1 Similarity 87.5%;
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTAACATCTATGTTTG 17
                   16
                             2 AGGAACCUCUAUGUUU 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACI60535 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 GTAATATATATGTTTG
                                                                                                                  23-JUN-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cross-species comparison.
                  1 AGTAACATCTATGTTT
                                                                                                                                                                                                                                                                               Backman KC, Carrino JJ,
  Conservative
                                                                                                                                                                                                                                                                                             WPI; 1992-073668/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                             (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-0CT-2003
                                                                                                                                                                                                                           29-AUG-1991;
                                                                                                                                                                                                                                            30-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ21862-78
   8
                                                                                                                                                                                                        04-MAR-1992
                                                                                                                                                                                        EP473155-A.
                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACI60535;
                                                                                                 AAQ21867;
                                                                                                                                                                                                                                                                                                                                    sambles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 16
                                                                      Matches
                                                               RESULT 15
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Compounds an expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation to a DNA library, or at least one target sequence. The method of analysis comprises of at least one rarget sequence. The method of analysis comprises of at least one or more nucleic acid probes are specifically designed for analysis of at least one or more nucleic acids to at least two or more nucleic acid probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises of the array of nucleic acids further comprises of the sequence or specific probes is useful in in situ hybridisation, in Southern, Northern or dotor mutations of any gene, in mapping the 5' termini of mRNA molecules by containing segments of DNA that have been containing segments of DNA that have been contained and previously sequenced. The sequence presented is one of the solute for this patent can also be obtained in electronic format directly compared in the microarray. Note: The sequence of the data for this patent can also be obtained in electronic format directly the sequence of the data for this patent sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human microarray DNA oligonucleotide SEQ ID NO 1523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25 BP; 6 A; 4 C; 5 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 60526; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACI01532 standard; DNA; 25 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16
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15-MAR-2002; 2002US-00098263.
                                                                                                               16-MAR-2001; 2001US-0276759P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 87.5%;
Matches 14; Conservative
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08-AUG-2002; 2002US-00215112. 08-AUG-2001; 2001US-0311040P.

US2003082596-A1.

01-MAY-2003

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The present libration letaces to muchato actual sequences that are compelementary to particular genes, and can be used as probes for a variety of analyses such as gene expression analysis. Each probe compenses 9 or more consecutive nuclectides from at least one of 14936 nucleotide sequences defined in the patent, or their perfect sense match, sense mismatch, antisense match or antisense match or antisense match of an instance of a monitoring gene expression concleic acid probes. The array is useful in monitoring gene expression levels by hybridisation to a DNA library, in analysing genetic variations, and in hybridisation are labelled compounds. The probes are also useful in in situ hybridisations, in screening companions are also cuseful in in situ hybridisations. In screening containing segments of DNA that have been previously isolated and sequenced, in Southern, northern, or det-blot hybridisation of genomic DNA to identify or detect the sequence of any gene or detect specific mutations in any gene, and in mapping the 5' termini of mRNA molecules by primer extensions. The mapping the 5' termini of mRNA molecules by primer extensions. The mapping the sylvaticular genes with a wide range of analytical uses. Complementary to particular genes with a wide range of analytical uses. The analytical uses of the invention provides a large collection of mucheces of the invention. Note:
               The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its operfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression nalysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises compounds are attached to a solid support. The analysis comprises molectic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acids further comprises a tag sequence. The array of nucleic acids further comprises a tag sequence or specific contactions of any gene, in mapping the 5' termini of mRNA molecules by comparisons or in screening contactions of any sequenced. The sequence or specific for additional subclones containing segments of DNA that have been contained and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence or sequence and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence or sequence and previously sequence. The microarray is sequence. The sequence or sequence and previously sequenced. The sequence presented is one of the sequence or sequence. The sequence or sequence or sequence or sequence or sequence or sequence. The sequence or sequence or sequence or sequence or sequence or sequence or sequence. The sequence or sequence or sequence or sequence 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1523; 9pp; English.
                                                                                                                                                       15-MAR-2002; 2002US-00098263.
                                                                                                                                                                                                                                   16-MAR-2001; 2001US-0276759P.
                                                                                                                                                                                                                                                                                                          (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-567953/53.
US2003104410-A1.
                                                                                                                                                                                                                                                                                                                                                                                      Mittmann MP;
                                                                           05-JUN-2003
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New probe array useful e.g. for monitoring gene expression levels, for analyzing genetic variations, or for hybridizing tag-labeled compounds, comprises multiple nucleic acid probes.

WPI; 2003-576608/54.

Mittmann M;

(MITT/) MITTMANN M.

present invention relates to nucleic acid sequences that are

The

Claim 1; SEQ ID NO 10981; 9pp; English

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Gene expression analysis, array; hybridisation, genetic variation, tag-labelled compound; gene family; in situ hybridisation; library screening; Southern hybridisation; northern hybridisation; dot-blot hybridisation; gene sequence; mutation detection; target sequence; probe; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                DNA target sequence #6520 useful in array for genetic analyses.
                                           ch 64.0%; Score 12.8; DB 8; Length 25;
l Similarity 87.5%; Pred. No. 1.6e+04;
14; Conservative 0; Mismatches 2; Indels
Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                     ACH57384 standard; DNA; 25 BP
                                                                                                                                  4 AACATCTATGTTTGGT 19
                                                                                                                                                           AACTICTATGTTTGCT 19
                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            16-0CT-2003
                                                                                                                                                                                                                                                                                                                                ACH57384;
                                                                                       Matches
                                                                                                                                                                                                                                         RESULT 19
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                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene expression analysis, array; hybridisation; genetic variation; tag-labelled compound; gene family; in situ hybridisation; library screening; Southern hybridisation; northern hybridisation; dot-blot hybridisation; gene sequence; mutation detection; target sequence; probe; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                            DNA target sequence #10981 useful in array for genetic analyses.
                                                                                    .,
                                  64.0%; Score 12.8; DB 8; Length 25; 87.5%; Pred. No. 1.6e+04; ive 0; Mismatches 2; Indels
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ACH61845 standard; DNA; 25 BP.

RESULT 18 ACH61845 (first entry)

17-0CT-2003 ACH61845;

Unidentified

19 16

4 AACATCTATGTTTGGT 1 AACGICTATCTTIGGT

à 셤

Query Match Best Local Similarity 87.5%; Matches 14; Conservative

Unidentified

.. 0

Gaps

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The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html

28-JUN-2001

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08-AUG-2002; 2002US-00215112.
              08-AUG-2001; 2001US-0311040P
                   (MITT/) MITTMANN M.
                                                                                                                                                                              Avena strigosa.
                                                                                                                                                                                   WO200146391-A2.
US2003082596-A1
                                                                                                                                                         24-OCT-2001
     01-MAY-2003
                         Mittmann M;
                                                                                                                                                    AAS09822;
                                                                                                                   Query Match
                                                                                                                                          Matches
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The present invention relates to nucleic acid sequences that are complementary to particular genes, and can be used as probes for a variety of analyses such as gene expression analysis. Each probe comprises 9 or more consecutive nucleotides from at least one of 14936 nucleotide sequences defined in the patent, or their perfect sense match, sense mismatch, antisense match or antisense mismatch oligonucleotides. The probes may be used in an array comprising at least 10 distinct mucleic acid probes. The array is useful in monitoring gene expression levels by hybridisation to a DNA library, in analysing genetic cusful for identifying family members of a gene. The probes are also useful in in situ hybridisations, in screening cDNA or genomic libraries (or derived subclones) for additional clones containing sequents of DNA that have been previously isolated and sequenced, in Southern, northern, or dot-blot hybridisation of genomic DNA to identify or detect the sequence of any gene or detect specific mutations in any gene, and in mapping the 5' termini of many molecules by primer extensions. The sequences of the invention are also useful as PCR primers.

Complementary to particular genes with a wide range of analytical uses. ACH50855-ACH65260 represent the target sequences of the invention. Note: The sequence data for this patent was obtained in electronic format correctly from the USPTO web site at sequences. New probe array useful e.g. for monitoring gene expression levels, for analyzing genetic variations, or for hybridizing tag-labeled compounds, comprises multiple nucleic acid probes. Claim 1; SEQ ID NO 6520; 9pp; English WPI; 2003-576608/54.

à ö Gaps ; 0 64.0%; Score 12.8; DB 8; Length 25; 87.5%; Pred. No. 1.6e+04; tive 0; Mismatches 2; Indels Sequence 25 BP; 6 A; 4 C; 4 G; 11 T; 0 U; 0 Other; 1 Similarity 87.5%; 14; Conservative Local Similarity

4 AACAICIAIGIIIGGI 19

AAS09822 standard; DNA; 30 BP (first entry)

Oat Beta-amyrin synthase sequencing primer 64.

Oat, Beta-amyrin synthase; triterpenoid, palatability, oxidosqualene cyclase; pathogen resistance; transgenic plant; fungal disease; sequencing primer; ss.

The sequence represents a primer used to sequence nucleic acids encoding CC Oat Beta-amyrin synthase (an oxidosqualene cyclase). Beta-amyrin is a triterpenoid responsible for paltablity to animals and resistance to pathogens and predators. The beta-amyrin synthase encoding nucleic acid is useful for producing a transgent plant, by introducing a vector containing it into a host cell, optionally causing or allowing crecombination between the vector and the host cell genome so as to transform the host cell, and regenerating a plant from the transformed plant cell. The DNA is also useful for identifying, cloning or determining the presence of a nucleic acid in a sample and for influencing or affecting the quantity or quality of triterpenoid synthesis, preferably an oleanane-type triterpene saponin synthesis, in a scomycete having a strond-containing membrane, optionally selected from ascomycete parting resistance to a fungal pathogen e.g., an accomycete parting vars tritici and avenae, fusarium culmorus, F. Gaeumannomyces graminis vars tritici and avenae, fusarium culmorus, F. CC avanaceum, Stagonospora nodorum or S. avenae, taste, palatability and/or nutritional value, of the plant, by causing or allowing expression of the for reducing the level of trierpenoids in the plant, by causing or allowing expression from an antisense molecule in the plant, allowing transcription from the DNA, or its part such as to reduce beta-amyrin cyluboryme specific for the DNA Novel beta-amyrin synthase encoding nucleic acids useful for influencing or affecting triterpene synthesis, and hence resistance to fungal pathogen, taste, palatability or nutritional value of plants. Bryan GT; Example 4; Page 60; 69pp; English. Haralampidis K, 20-DEC-2000; 2000WO-GB004908. 16-AUG-2000; 2000GB-00020217. 99GB-00030394 (PLAN-) PLANT BIOSCIENCE LTD WPI; 2001-418055/44. 22-DEC-1999; Osbourn AE, 

ö Gaps ö Query Match

64.0%; Score 12.8; DB 4; Length 30;
Best Local Similarity 87.5%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels

Sequence 30 BP; 7 A; 8 C; 4 G; 11 T; 0 U; 0 Other;

g

RESULT 21 AAF83283

AAF83283 standard; DNA; 34 BP 09-JUL-2001 (first entry) AAF83283;

Human Chkl DNA amplifying primer chk6w.

Effector checkpoint protein kinase; Chk1; hyperproliferation; HIV; cancer; cytostatic; anti HIV; gene therapy; PCR primer; ss.

EP1096014-A2.

02-MAY-2001

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The invention relates to an isolated, soluble, catalytically active human effector checkpoint protein kinase (Chk1) polypeptide. Chk1 protein can be expressed by standard recombinant methodology. Chk1 is useful for screening for its inhibitors, used for treating hyperproliferative diseases, such as, HIV and cancer. The Chk1 DNA is useful for probes, primers, chemical intermediates, and in biological assays. Sequences AAF83283-290 represent PCR primers for amplifying the human Chk1 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of
                                                                                                                                                                                                           Novel isolated, soluble, catalytically active human effector checkpoint protein kinase, useful for screening inhibitors of hChk1 kinase, for treating hyperproliferative disorders such as HIV and cancer.
                                                                                                                           Tempczyk-Russel A;
Lundgren K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal; PCR; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Candida essential gene related knockout PCR primer SEQ ID NO 1712.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.0%; Score 12.8; DB 4; Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                       n C, Luo C, Margosiak S, O'connor P, Tv
Sarup JC, Gaur S, Anderson MB, Deng Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohlsen KL;
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 34 BP; 6 A; 7 C; 7 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.6e+04;
0; Mismatches 2
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                                                                                                                                                                                                                                                                     Example 2; Page 15; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABZ27765 standard; DNA; 43 BP
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               31-OCT-2000; 2000EP-00123738
                                             99US-0162887P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-DEC-2000; 2000US-0259128P.
20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AGTAACATCTATGTTT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.5%;
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                                                                                        (AGOU-) AGOURON PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 87.5
les 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                  WPI; 2001-302195/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roemer T, Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-566694/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Candida albicans
                                                                                                                       Kan C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200253728-A2.
                                            01-NOV-1999;
14-DEC-1999;
                                                                                                                                                    Register J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUL-2002.
                                                                                                                                      Nguyen B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABZ27765:
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                                                                                                                       Chen P,
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Matches
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The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying cells in which both alleles of a gene are modified, comprising modifying constants assette having an expressible selectable marker and modifying other allele by insertion or replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles modified are useful for identifying a gene that cells in which both alleles modified are useful for identifying a gene that cells in which beth alleles modified are useful for identifying a gene that contributes to the survival or growth of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent that inhibits the growth of a diploid fungus agent, an antifungal agent that inhibits the growth of a diploid fungus or and for identifying a compound without activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transporter, transcriptional, compound catabolism, signal transduction, DNA replication and cell division attivity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of a pCR primer used in the method of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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gene and placing other allele of the gene under conditional expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomic map; haplotype; phenotype; polymorphic base; genotyping;
haplotyping; hybridisation; identification; characterisation; diagnosis;
single nucleotide polymorphism; SNP; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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/standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome; biallelic marker; high density disequilibrium map;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
                                      Claim 76; SEQ ID NO 1712; 167pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.0%; Score 12.8; DB 6; Length 43; 87.5%; Pred. No. 1.6e+04; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 43 BP; 24 A; 4 C; 3 G; 12 T; 0 U; 0 Other;
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replace(24,C)
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98US-0109732P.
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AAZ67540 standard; DNA; 47
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Best Local Similarity
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23-NOV-1998;
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Chumakov I;

Novel biallelic markers used to construct a high density disequilibrium Claim 1; Page 633; 2745pp; English. ABL00484 standard; DNA; 51 BP (first entry) Blumenfeld M, map of the human genome Query Match Best Local Similarity WPI; 2000-013267/01 present invention WO200138586-A2 24-NOV-1999; Homo sapiens 05-MAR-2002 31-MAY-2001. ABL00484; Cohen D, Matches ABL00484/6

IID ABL00

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ABL00

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Human

DE Human

DE Human

EN Human

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invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallellic markers. The biallellic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential effications responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment. N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the AAZ65654 to AAZ69578 represent human biallelic markers from the present Gaps . 0 64.0%; Score 12.8; DB 3; Length 47; 87.5%; Pred. No. 1.7e+04; 2; Indels Sequence 47 BP; 22 A; 5 C; 4 G; 16 T; 0 U; 0 Other; 0; Mismatches 5 ACATCTATGTTTGGTT 20 l Similarity 87.5%; 14; Conservative

43 ACATTTATGTTTGTTT 28

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Human silent noncoding SNP oligonucleotide SEQ ID NO:475.

Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic; immunosuppressive; antiinflammatory; neuroprotective; antimicrobial; autoimmune disease; inflammation; cancer; nervous system disease; inflection; polymorphic protein; ds.

22-NOV-2000; 2000WO-US032311.

99US-0167383P

(CURA-) CURAGEN CORP.

WPI; 2001-355949/37.

Leach M;

Shimkets RA,

Isolated human nucleic acids comprising one or more single nucleotide polymorphisms, useful for treating a subject suffering from a pathology, e.g. autoimmune diseases, ascribed to the presence of a sequence polymorphism.

This invention describes a novel avian-paramyxovirus cDNA (I) which comprises a nucleic acid sequence corresponding to the 5' terminal end of the genome of avian-paramyxovirus allowing the generation of an infectious copy of avian-paramyxovirus. The cell line is useful for the production of infectious lentogenic NDV (Newcastle Disease virus) without the addition of exogenous proteolytic activity. Also it is possible to generate a stable transfected cell line that expresses the wild-type F protein in the virus envelope therefore providing infectious particles, useful in the form of a vaccine, especially against respiratory and/or

New avian paramyxovirus cDNA, useful for production of vaccine against

Disclosure; Page 33; 115pp; English.

disease virus

Newcastle

Gielkens ALJ

Koch G,

Peeters BPH, De Leeuw OS,

WPI; 2000-106102/09.

(DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE.

99WO-NL000377. 98EP-00202054.

19-JUN-1998; 17-JUN-1999; 23-DEC-1999.

local immunity; primer; ss.

Newcastle disease virus.

W09966045-A1.

Claim 1; Page 391; 674pp; English

comprising one or more single nuclectide polymorphisms (SNP8). ABB56531

comprising one or more single nuclectide polymorphisms (SNP8). ABB56531

coligonuclectides. The sequences from the present invention can have immunosuppressive, cytostatic, antiniflammatory, neuroprotective and antibodies from the present invention can be used for treating a and antibodies from the present invention can be used for treating a subject suffering from, at risk for, or suspected of, suffering from a cubject suffering from a fasease, inflammation, cancer, diseases of pathology may be autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. The SNPs are also useful for determining which forms of a characterised to polymorphism are present in individuals. The antibodies may be used in the detection, quantitation and/or cellular or tissue localisation of a polymorphic protein (e.g., for use in measuring levels of the polymorphic protein (e.g., for use in measuring levels of the polymorphic . 0 Gaps ABL00010 to ABL01104 represent human nucleic acid oligonucleotides Avian-paramyxovirus; infection; lentogenic; F protein; vaccine; respiratory disease; gastrointestinal disease; poultry pathogen; ; Score 12.8; DB 5; Length 51; Pred. No. 1.7e+04; Indels Sequence 51 BP; 11 A; 12 C; 13 G; 15 T; 0 U; 0 Other; Newcastle disease virus LaSota primer BGL5F2. 0; Mismatches AAZ44622 standard; DNA; 58 BP 64.0%; 87.5%; 3 TAACATCTATGTTTGG 18 38 raacarcrargagieg 23 07-APR-2000 (first entry) Ouery Match Best Local Similarity 87.5 Matches 14; Conservative AAZ44622; RESULT 25 AAZ44622, 셤 \*555555555555555555588 ò

analysis of S. cerevisiae YOL077C knock-out mutant

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Gaps

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The invention relates to genes in S. cerevisiae which are essential for germination and proliferation. The essential genes (EG) such as YDR141C, YDR091C, YOLO26C, YOLO34W and YOL077C are used in a method for identifying potential antifungal compounds (CP). The method comprises overexpressing the EG cells, isolating a subset of genes induced to repressed by overexpression of EG and determining effect of Cp on down/up requilation of any subset of genes or contacting a protein encoded by EG with Cp and determining binding between them. Cp is identified as a potential antifungal Cp, if it downregulates a gene that is induced by coverexpression of EG or if it downregulates a gene that is induced by coverexpression of EG or if it upregulates the gene that is repressed by the method is useful for identifying novel antifungal compounds for treating fungal diseases and proliferative discorders in human and nontum mammals, including monkeys and other primates, dogs, cats.

Sequences AAFB623273-280 represents PCR primares for the construction and
gastrointestinal diseases. NDV can be easily cultured to very high titers in embryonated eggs. Mass culture of embryonated eggs is relatively cheap. NDV vaccines are relatively stable and can be simply administered by mass application methods e.g. drinking water or by spraying or by acrosol formation. The natural route of infection is by the respiratory and/or gastrointestinal tract which are also the major routes of infection of many other poultry pathogens. NDV can induce local immunity despite the presence of circularing maternal antibody. AAZ44527-Z44609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Germination; proliferation; essential gene; YDR141C; YDR091C; YOL026C;
YOL034W; YOL077C; antifungal; fungal disease; YOL022C; antisense therapy;
mutant; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying antifungal compounds for treating fungal and proliferative diseases, by using yeast genes essential for germination and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S. cerevisiae YOL077C knock-out mutant constructing primer UPTAG.
                                                                                                                                                                                                                                                                          Length 58;
                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                              Sequence 58 BP; 21 A; 11 C; 11 G; 15 T; 0 U; 0 Other;
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Pred. No. 1.7e+04;
                                                                                                                                                                                                                                                                                                            0; Mismatches
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1 Similarity 87.5%;
14; Conservative (
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                                                                                                                                                                                          strain LaSota genome
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                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                           Microarray; probe; Mycobacterium; antibiotic-resistance; genotyping; ss.
                                                                                             Gaps
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                                                         Query Match 64.0%; Score 12.8; DB 4; Length 74; Best Local Similarity 87.5%; Pred. No. 1.7e+04; Matches 14; Conservative 0; Mismatches 2; Indels
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                             Sequence 74 BP; 18 A; 20 C; 20 G; 16 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                              marinum - M ulcerans specific probe MAR-ULC-02.
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                                                                                                                                                     23 ACATCCATCTTTGGTT 8
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Best Local Similarity 78.9
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium marinum.
Mycobacterium ulcerans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003031654-A1.
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ID AAX026
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AAX02618 standard; DNA; 24 BP.

EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;

cross-species comparison

US2003104410-A1. Homo sapiens.

05-JUN-2003

15-MAR-2002; 2002US-00098263. 16-MAR-2001; 2001US-0276759P.

(AFFY-) AFFYMETRIX INC

WPI; 2003-567953/53.

Mittmann MP;

Human microarray DNA oligonucleotide SEQ ID NO 128010.

(first entry)

14-OCT-2003

ACK28029

(first entry)

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S. aureus SecA2 PCR primer #1.
   07-MAY-1999
            Synthetic
AAX02618;
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This invention describes the isolation of a novel Staphylococcus aureus ATPase subunit of preprotein translocase (SecA). SecA polypeptides and polymerolecides are useful for diagnosing diseases related to over or underexpression of SecA protein by identifying mutations in the SecA gene, or determining SecA polypeptide or mRNA expression levels due to an infection of an organism with the SecA gene. They can diagnose the stage infection of an organism with the SecA gene. They can diagnose the stage of infection. SecA polypeptides can be used in treatment to inhibit (antagonist i.e. antibacterial drugs) or enhance (agonist) SecA critisty. Diseases diagnosed, prevented or treated include bacterial infections, especially Staphylococcus aureus infections of the upper and lower respiratory tract (e.g. otitis media, thyroiditis), cardiac (e.g. infections of endocarditis), gastrointestinal (e.g. secretory diarrhoes, infections), kidney and urinary tract (e.g. toxic shock syndrome), skin (e.g. impetigo, wound infection), and bone and joint (e.g. septic arthritis, osteomyelitis). SecA polypeptides, polynucleotides and their (ant)agonists can prevent adhesion of bacteria to matrix proteins) are useful for use on wounds and body implants to prevent bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Staphylococcus aureus ATPase subunit of preprotein translocase (SecAs) polypeptide and polymuclostide - useful as diagnostic reagents and for prevention and treatment of Staphylococcus aureus infections, including toxic shock syndrome and splenic abscess.
                                    treatment; inhibit; antagonist; agonist; disease; bacterial; cardiac; respiratory tract; gastrointestinal; central nervous system; CNS; eye; kidney; urinary tract; skin; bone; joint; bacterial adhesion; wound; matrix proteins; body implant; PCR primer; ss.
SecA2; ATPase subunit; preprotein translocase; diagnosis; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24 BP; 11 A; 3 C; 4 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus.
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New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 128010; 9pp; English

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises thybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dotblot hybridisation to identify or detect the sequence or specific or mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening segments of DNA that have been to repet in source or specific or isolated and previously sequence. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.goc/sequence.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACI29919 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Conservative
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AC129919/c
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AC AC1299:
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Gaps

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63.0%; Score 12.6; DB 2; Length 24; 78.9%; Pred. No. 2e+04; cive 0; Mismatches 4; Indels

2 GTAACATCTATGTTTGGTT 20

15; Conservative

Similarity

Local

Matches

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Query Match

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GTAACATCTAGTTTATGTT

ACK28029 standard; DNA; 25 BP.

ACK28029/c ID ACK28 XX

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, and analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence in the method of analysis comprises of hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific concluded any gene, in mapping the 5' termini of mand molecules by the primar extensions or in screening cDNA or genomic libraries or subclones confatiling segments of bNA that have been contacted the contacted or any sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at segdata.uspto.goc/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                       EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
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                                        Human microarray DNA oligonucleotide SEQ ID NO 29910.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 29910; 9pp; English.
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                                                                                                                                                                                                                                                                                                                                                 16-MAR-2001; 2001US-0276759P.
                                                                                                                                                                                                                                                                                                       15-MAR-2002; 2002US-00098263.
(first entry)
                                                                                                                                cross-species comparison.
                                                                                                                                                                                                                                                                                                                                                                                          (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-567953/53.
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Les 15; Conserv
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                                                                                                                                                                           sapiens.
  13-OCT-2003
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Gaps .. 63.0%; Score 12.6; DB 8; Length 25; llarity 78.9%; Pred. No. 2e+04; Conservative 0; Mismatches 4; Indels 19 AGTAACATCAAAGTCTGTT 1

BP. ACI36381 standard; DNA; 25 (first entry) 13-OCT-2003 ACI36381; ACT36381/c 1D ACT3638 XX AC ACT3638 XX DT 13-OCT RESULT 31

ss; probe; expressed sequence tag; microarray; gene expression; ic variation; biallelic marker; polymorphism; human; Human microarray DNA oligonucleotide SEQ ID NO 36372. cross-species comparison. genetic variation; 

Homo sapiens.

JS2003104410-A1.

05-JUN-2003

15-MAR-2002; 2002US-00098263.

16-MAR-2001; 2001US-0276759P.

(AFFY-) AFFYMETRIX INC

Mittmann MP;

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 36372; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises for uncleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, cor family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid further comprises to a green and a cross-species comparison. Each of the concleic acids further comprises to tag sequence. The array of nucleic acid further comprises to the sequence or specific comparations of any gene, in mapping the 5' termini of mRNA molecules by complement subclones containing segments of DNA that have been contained and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence contained and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence contained to the sequence contained in electronic format directly from USPTO at sequence. Then also be obtained in electronic format directly from the sequence of the contained in electronic format directly from the contained in electronic format directly from the contained in electronic format directly from the contained in the microarray.

Sequence 25 BP; 9 A; 4 C; 5 G; 7 T; 0 U; 0 Other;

Gaps ; 0 63.0%; Score 12.6; DB 8; Length 25; 78.9%; Pred. No. 2e+04; Score Lar.,
Pred. No. 2e+04; 0; Mismatches Best Local Similarity 78.9 Matches 15; Conservative Query Match

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Human microarray DNA oligonucleotide SEQ ID NO 65195. (first entry) 13-OCT-2003 ACI65204; XEXEX

ACI65204 standard; DNA; 25 BP.

RESULT 32 ACI 65204

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in bybridisation to a DNA library. CC in analysis of genetic variation or in bybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring concern expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid subport in situ hybridisation, in Southern, Northern or dotonce is useful in in situ hybridisation, in Southern, Northern or dotonce additional subclones containing segments of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and probes incorporated in the microarray. Note: The sequence date for this patent can also be obtained in electronic format directly from the containing the sequence them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 65195; 9pp; English.
                                                                                                                                                                                                                                15-MAR-2002; 2002US-00098263.
                                                                                                                                                                                                                                                                          16-MAR-2001; 2001US-0276759P
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                                                                                                                                           US2003104410-A1
                                                                                                Homo sapiens.
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                        Score 12.6; DB 8; Length 25; Pred. No. 2e+04; 0; Mismatches 4; Indels
Sequence 25 BP; 4 A; 4 C; 8 G; 9 T; 0 U; 0 Other;
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0
                        63.0%;
78.9%;
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                                       Local Similarity
Les 15; Conserv
                            Query Match
                                                   Matches
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GTAACATCTATGTTTGGTT 20
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ACK00121 standard; DNA; 25
                                                           (first entry)
                                                           14-OCT-2003
                                       ACK00121;
RESULT 33
         ACK00121

ID ACK

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AC ACK

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BP.

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Human microarray DNA oligonucleotide SEQ ID NO 100102.
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EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation to a DNA library, in analysis of genetic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises of hybridising at least one or more nucleic acid statements. The nucleic acid probes and detecting the hybridisation. The nucleic acid forces are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dotblot hybridisation to identify or detect the sequence or specific or mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or an screening segments of DNA that have been consolations acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly concluded in electronic format directly concluded in the microarray. New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene. Sequence 25 BP; 5 A; 7 C; 5 G; 8 T; 0 U; 0 Other; Claim 1; SEQ ID NO 100102; 9pp; English 15-MAR-2002; 2002US-00098263. 16-MAR-2001; 2001US-0276759P. cross-species comparison. (AFFY-) AFFYMETRIX INC. WPI; 2003-567953/53. US2003104410-A1. Homo sapiens. Mittmann MP; 05-JUN-2003 

Gaps 0; 63.0%; Score 12.6; DB 8; Length 25; 78.9%; Pred. No. 2e+04; ive 0; Mismatches 4; Indels Best Local Similarity 78.9 Matches 15; Conservative Query Match

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1 AGTAACATCTATGTTTGGT 19
                          AGTACCATCTACGTTCCGT 21
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ð 셤 ACI27083 standard; DNA; 25

ACI27083;

EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison. Human microarray DNA oligonucleotide SEQ ID NO 27074. (first entry) 13-OCT-2003 

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, or nanitoring gene expression levels by hybridisation to a DNA library, or property and probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring compensation levels, identifying biallelic markers or polymorphisms, or family members of a gene across-species comparison. Each of the nucleic acids further comprises at an sequence. The array of nucleic acid control of an across-species comparison. Each of the nucleic acids further comprises at an sequence. The array of nucleic acids further comprises at an sequence or specific acid control of an across-species comparison of a control of an across-species comparison. Each of the mutations of any gene, in mapping the 5' termin of mRNA molecules by thimer extensions or in screening cNNA or genemanic libraries or subclones for a shift control such and a cross-species or subclones.
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                                                                                                                                                                                                                                                                                                                                                                                                        New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 27074; 9pp; English.
                                                                                                                                                L5-MAR-2002; 2002US-00098263.
                                                                                                                                                                                                     16-MAR-2001; 2001US-0276759P.
                                                                                                                                                                                                                                                     (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-567953/53.
                                                US2003104410-A1.
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Homo sapiens.
                                                                                                05-JUN-2003.
                                                                                                                                                                                                                                                                                                        Mittmann MP;
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its component match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by bybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis of genetic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises comprises the probes are attached to a solid support. The metalysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, cor family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific acid further comprises a tag sequence or specific acid further comprises a tag sequence or specific acid further comprises or the sequence or specific acid probes is useful in in situ hybridisation, in Southern, Northern or dottore hybridisation to identify or detect the sequence or specific acid probes in mapping the 5' termini of mRNA milecules by commutations of any gene, in mapping the 5' termini of mRNA milecules by commer extensions or in screening SONA or genomic libraries or subclones is solated and previously sequenced. The sequence presented is neceptated in the microarray. Note: The sequence or format directly from USPPO at sequence. The libraries or subclones and so be obtained in electronic format directly from the sequence or the sequenc

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

16-MAR-2001; 2001US-0276759P.

(AFFY-) AFFYMETRIX INC

WPI; 2003-567953/53.

Mittmann MP;

15-MAR-2002; 2002US-00098263.

US2003104410-A1

05-JUN-2003

Claim 1; SEQ ID NO 35736; 9pp; English.

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Score 12.6; DB 8; Length 25; Pred. No. 2e+04; 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                           Sequence 25 BP; 9 A; 4 C; 5 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                     1 AGTAACATCTATGTTTGGT 19
                                                                                                                                                                                                                                                                                                                                                                  24 AGTAACTICAATGICIGIT 6
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                                                                                                                                                                                                                                                                                                                         63.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Best Local Similarity 78.9
Matches 15; Conservative
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Local Similarity

Matches

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Gaps

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EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                     Human microarray DNA oligonucleotide SEQ ID NO 25123.
                                                                                                 cross-species comparison.
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                                                                                                                         Homo sapiens.
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ss; probe; expressed sequence tag; microarray; gene expression; ic variation; biallelic marker; polymorphism; human;

cross-species comparison.

genetic

Homo sapiens

Human microarray DNA oligonucleotide SEQ ID NO 35736.

13-OCT-2003

ACI35745;

ACI35745/c

RESULT 35

16-MAR-2001; 2001US-0276759P 15-MAR-2002; 2002US-00098263

(AFFY-) AFFYMETRIX INC.

WPI; 2003-567953/53

Mittmann MP;

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in manlysis of genetic variation or in hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises in hybridising at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Bach of the nucleic acids further comprises a tay sequence. The array of nucleic acid further comprises a tay sequence. The array of nucleic acid further comprises a tay sequence. The array of nucleic acid further comprises a tay sequence. The array of nucleic acid for any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Noce: The sequence containing the contain
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                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 25123; 9pp; English.
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                                                                                               16-MAR-2001; 2001US-0276759P.
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                                           15-MAR-2002; 2002US-00098263
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                                                                                                                                                (AFFY-) AFFYMETRIX INC
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05-JUN-2003
                                                                                                                                                                                                 Mittmann MP
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in manitoring gene expression levels by hybridisation to a DNA library, and nonitoring gene expression levels by hybridisation to a DNA library, of a nanitysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of the least one target sequence. The method of analysis comprises for nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring concern attached to a solid support. The analysis comprises monitoring can expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a torge species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid sorbes is useful in in situ hybridisation, in Southern, Northern or dotbrobe the hybridisation to identify or detect the sequence or specific mitations of any gene, in mapping DNA or genemic libraries or subclones for additional subclones when have hear

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 35597; 9pp; English.

for additional subclones containing segments of DNA that have been isolated and previously segmenced. The segmence presented is one of the nucleic acid probes incorporated in the microarray. Note: The segmence data for this patent can also be obtained in electronic format directly

Sequence 25 BP; 4 A; 5 C; 7 G; 9 T; 0 U; 0 Other; from USPTO at segdata.uspto.goc/sequence.html

Gaps . 0

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ASTH1; asthma; human; chromosome 11p; ASTH11; ASTH1J; genetic locus; ss; therapeutic; immunogen; polymorphism; PCR primer; microsatellite marker.
Query Match 63.0%; Score 12.6; DB 8; Length 25; Best Local Similarity 78.9%; Pred. No. 2e+04; Matches 15; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                Primer for ASTH1 polmorphic microsatellite marker.
                                                                  2 GTAACATCTATGTTTGGTT 20
                                                                                                 Graacaggragerricerr 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US001260.
                                                                                                                                                                   AAZ18573/c
ID AAZ18573 standard; DNA; 27
                                                                                                                                                                                                                                                19-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-1999.
                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                 AAZ18573;
                                                                                                                                                    RESULT 38
                                                                                                                                                                                    g
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                                                                                                                                                                                                                                                                                                                                               EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                                                                                 Human microarray DNA oligonucleotide SEQ ID NO 35597.
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BP

ACI35606 standard; DNA; 25

(first entry)

13-0CT-2003

ACI35606;

cross-species comparison

JS2003104410-A1 Homo sapiens

05-JUN-2003

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                                                                                                                                                              mapped to human chromosome 110. ASTHII and ASTHII are genes present within the locus, located close to each other on human chromosome 11p, and have similar patterns of expression, and common sequence motifs. The ASTHI genes and fragments, encoded protein, agenomic regulatory regions and anti-ASTHI antibodies are useful in the identification of individuals predisposed to development of asthma, and for the modulation of gene activity in vivo for prophylactic and therapeutic purposes. The ASTHI protein is useful as an immunogen to raise specific antibodies, in drug screening for compositions that mimic or modulate ASTHI activity or expression, including altered forms of ASTHI protein, and as a therapeutic. Sequences AAZH8510-Z18631 represent POR primers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASTH1 polymorphic microsatellite marker AFMA154ZD1 primer, SEQ ID NO:223.
                                                                                                 Mammalian asthma related genes, useful for diagnosis of a predisposition to development of asthma.
                                                                                                                                                       The invention identifies a genetic locus ASTH1, associated with asthma,
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bronchial hyperreactivity; ets family; transcription factor; splice variant; genetic predisposition; polymorphism; antibody, drug screening; prophylaxis; therapy; diagnosis; polymorphic microsatellite marker flanking sequence; batched analysis of genotypes; BAGs; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                              .;
0
                                            Galvin M;
                                                                                                                                                                                                                                                                                                                                    63.0%; Score 12.6; DB 2; Length 27; 78.9%; Pred. No. 2e+04; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASTH1 locus; ASTH11; ASTH1J; human; chromosome 11p; asthma;
                                                                                                                                                                                                                                                                                           polymorphic microsatellite markers in the ASTH1 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buckler A;
                                            Carey AH,
                                                                                                                                                                                                                                                                                                                Sequence 27 BP; 5 A; 6 C; 6 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cardon L,
                                           Cardon L,
                                                                                                                                  Disclosure; Page 50; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  1 AGTAACATCTATGTTTGGT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 North M,
                                                                                                                                                                                                                                                                                                                                                                                                        27 AGTAACATCTCAGCCTGGT 9
                                           Buckler A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΗB
98WO-US001260.
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97US-0051432P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carey AH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA80480 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                 Local Similarity 78,9
                     (AXYS-) AXYS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AXYS-) AXYS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miller A,
                                                      Miller A, North M;
                                                                            WPI; 1999-479058/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-505109/45.
                                          Brooks-Wilson AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brooks-Wilson AR,
21-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6087485-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUL-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA80480;
                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                            Matches
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The invention relates to the ASTH1 locus on the short arm of human chromosome (11p). This locus comprises the ASTH1I and ASTH1J genes, which chromosome (11p). This locus comprises the ASTH1I and ASTH1J genes are oriented in opposite are associated with the ASTH1 and ASTH1J and batterns of expression and rections with the ASTH1 and ASTH1J are novel members of expression and common sequence motifs. They are both expressed in trached, lung and common sequence motifs. They are both expressed in trached, lung and common sequence motifs. They are both expressed in trached, lung and common sequence motifs. They are both expressed in trached, transcription factors, which have been implicated in the common sequence motifs. They are both expressed in trached, attentively spliced. Alternative splicing of ASTH1I muth a setiology of asthma. Both ASTH1I and ASTH1I mansoripts has no effect on the open reading frame of ASTH1J as the expression of the start codon in exon b. In contrast, a leoforms. The invention also encompasses mouse asth1j protein. The ASTH1I conclete acids are useful as dagnostics to identifying ASTH1 related genes, for identifying expression of the gene in a biological specimen, and for generating geneticinally modified non-human animals or site specific gene (modifications that aminc or modulate activity or expression of ASTH1I compositions that aminc or modulate activity or expression of ASTH1I compositions that aminc or modulate activity or expression of ASTH1I compositions that aminc or modulate activity or expression of ASTH1I compositions that aminc or modulate activity or expression of ASTH1I compositions that aminc or modulate activity or expression of ASTH1I compositions that aminc or modulate activity or expression of ASTH1I and as a theorem of activity in vivo for compositions that aminc or modulate forms of these proteins or reduce that the activity and activity and activity in vivo for prophylactic and therapeutic purposes. The intract ASTH1I and therapeutic purposes to favore also proteins or 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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New nucleic acids other than naturally occurring chromosomes encoding ASTH1 protein, for e.g. screening compositions that modulate expression or function of ASTH1 proteins or as diagnostics for genetic predisposition to asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27 BP; 5 A; 6 C; 6 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           batched analysis of genotypes (BAGs)
                                                                                                                                                                                                                                                   Example; Col 31-32; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGTAACATCTATGTTTGGT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACC72239/c
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SULT 40
CC72239/c
ACC72239 standard; DNA; 27 BP.
ACC72239;
O7-JUL-2003 (first entry)
Forward Ag7094 PCR primer.
Human; NOV; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective;

M immunomodulator; cytostatic; nootropic; neuroprotective;
M antiparkinsonian; antilipaemic; gene therapy; metabolic disorder;
W diabetes; obesity; inffection; cachexia; cancer; PCR; primer;
M neurodegenerative disorder; Alzheimer's disease;
W immune disorder; haematopoietic disorder; dyslipidaemia; ss.

S Homo sapiens.

WO2003029423-A2.

02-OCT-2001; 2001US-0326483P. 05-OCT-2001; 2001US-0327342P. 09-OCT-2001; 2001US-0327317P. 09-OCT-2001; 2001US-0328024P. 09-OCT-2001; 2001US-0328056P. 12-OCT-2001; 2001US-032814P. 15-OCT-2001; 2001US-0328414P. 17-OCT-2001; 2001US-0329414P. 17-OCT-2001; 2001US-0329414P. 22-OCT-2001; 2001US-0339266P. 24-OCT-2001; 2001US-0343629P.

02-OCT-2002; 2002WO-US031358

12-APR-2002; 2002US-0371980P.
17-APR-2002; 2002US-0373261P.
19-APR-2002; 2002US-0373665P.
23-APR-2002; 2002US-0374738P.
16-MXY-2002; 2002US-0381101P.
17-MXY-2002; 2002US-0381635P.
29-MAY-2002; 2002US-0383630P.

01-OCT-2002; 2002US-00262839

(CURA-) CURAGEN CORP.

2001US-0343629P. 2001US-0349575P. 2001US-0346357P. 2002US-0371972P.

01-NOV-2001; 29-OCT-2001; 12-APR-2002;

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CDNA sequence AAQ37477, encoding a neutrotrophic factor (NF), was derived from the native ciliary neurotrophic factor (CNTF) (e.g. EP-385060) by PCR amplification. In order to obtain a DNA sequence encoding the NF(1-180), a portion of the DNA sequence encoding AAs 76-180 of full-length CNTF was amplified using PCR from a bacterial expression vector, plasmid pSP18 and synthetic PCR primers AAQ37473 and AAQ37474. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homogeneous neurotrophic factor for treating neuro-degenerative diseases, e.g. Parkinsonism - comprise specified polypeptide sequence lacking micro-heterogeneity associated with a related native sequence factor.
                                                    to the sense strand for AAs 76-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.0%; Score 12.6; DB 2; Length 34; 78.9%; Pred. No. 2e+04; ive 0; Mismatches 4; Indels
                                                                                                              Neurotrophic factor; neuro-degenerative disease; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 34 BP; 5 A; 9 C; 5 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                    Thompson SA;
                                                    quence of PCR primer which corresp. ciliary neurotrophic factor (CNTF).
                                                                                                                                                                                                                                                                                                                                                                                    Cordell B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 bp spacer DNA used in aptamer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Page 14; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GTAACATCTATGTTTGGTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 Graccriccardrificati 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-NOV-2000; 2000US-0253097P.
                                                                                                                                                                                                                                                                  92WO-US007070.
                                                                                                                                                                                                                                                                                                        91US-00749446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK91114 standard; DNA; 50
                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                    Higaki JN, Tischer EG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aptamer; ss; sequencing
                                                                                                                                                                                                                                                                                                                                                (SCIO-) SCIOS NOVA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RIKE ) RIKEN KK.
(HAYA/) HAYASHIZAKI Y.
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-093724/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200244195-A2
                                                                                                                                                                                                                                                                      21-AUG-1992;
                                                                                                                                                                                                                                                                                                          23-AUG-1991;
                                                                                                                                                                                          WO9303758-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-NOV-2002
25-MAR-2003
03-JUL-1993
                                                                                                                                                                                                                                04-MAR-1993.
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                                                          Sequence of
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                                                                                                                                                      Synthetic
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ID ABK9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to novel human NOV proteins and their coding sequences (ACC72075-ACC72181 and ABR58363-ABR58469). The NOV proteins are useful in manufacturing a medicament for treating a syndrome associated with a human disease. The NOV proteins and coding sequences may be used to diagnose, treat or prevent metabolic disorders such as disbetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The present sequence is a PCR primer, used in an example from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOVX polypeptides and nucleic acids useful for diagnosing, preventing treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catterton E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Catterton E; Edinger SR, Ellerman K, Gerlach VL, Gorman L, Guo X, Ji W; Kekuda R, Leach MD, Li L, Miller CE, Patturajan M, Rieger DK; Rothenberg ME, Shinkers RA, Smithson G, Spytek KA, Taupier RJ; Vernet CAM, Voss EZ, Zerhusen BD, Zhong M;
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Seguence 27 BP; 10 A; 5 C; 4 G; 8 T; 0 U; 0 Other;

1 AGTAACATCTATGTTTGGT 19

Best Local Similarity

Matches

à g

Query Match

S

arraacarcarrerareer

AAQ37473 standard; DNA; 34 BP.

RESULT 41

AAQ37473

AAQ37473 ID AAQ3 XX AC AAQ3 XX

Example C; Page 360; 487pp; English

pharmacogenomics

WPI; 2003-381625/36

ö

Gaps

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K, Matcuk G, Altman P, P:
Quertermous T, Johnson F;
                                                     Example 4; Page 23; 56pp; English.
                                                                                                                                                                                                         1 AGTAACATCTATGTTTGGT 19
                                                                                                                                                                                                                     21 AGIGICATCIAIGICGGGI 3
                                                                                                                                                                                                                                                   ABZ00880 standard; DNA; 50 BP
                                                                                                                                                                                                                                                                                                                                                                               20-OCT-2000; 2000US-0241994P.
08-JUN-2001; 2001US-0296764P.
                                                                                                                                                                                                                                                                                                                                                                   22-OCT-2001; 2001WO-US047856.
                                                                                                                                                                                                                                                                          09-JAN-2003 (first entry)
                                                                                                                                                                                              15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  (BIOC-) BIOCARDIA INC.
                                                                                                                                                                                                                                                                                                                                                                                                              nuth J, Fry K,
Woodward R, Qu
                 WPI; 2002-608230/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-636525/68.
                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                           WO200257414-A2.
     Hayashizaki Y;
                                                                                                                                                                                                                                                                                                                                                                                                             Wohlgemuth J,
                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                               ABZ00880;
                                                                                                                                                                                 Query Match
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                                                                                                                                                                                        Best Loca
Matches
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The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ008152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T7; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human leukocyte gene expression profiling probe SEQ ID NO 3285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 12.6; DB 6; Length 50;
Pred. No. 2.1e+04;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prentice J,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 50 BP; 12 A; 10 C; 11 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johnson F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Altman P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fry K, Matcun J,
d R, Quertermous T,
                                                                          Claim 1; Page 352; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AGTAACATCTATGTTTGGT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 AGAACACCCTTGTTTGGT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABZ03294 standard; DNA; 50 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-OCT-2001; 2001WO-US047856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-OCT-2000; 2000US-0241994P. 08-JUN-2001; 2001US-0296764P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 63.0°
Best Local Similarity 78.9°
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-636525/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wohlgemuth J, Fry Ly N, Woodward R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200257414-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to novel isolated aptamers comprising at least one base capable of base pairing and different from the standard Watson-Crick (W-C) bases. The invention also comprises a method for sequencing nucleic acids. The aptomers of the invention are useful for isolating a specific acids. The aptomers of the invention are useful for isolating a specific ligand from a pool of ligands, by providing at least one specific aptamer. The aptomers of the invention are useful for detection of specific ligand from a biological sample, by selecting at least one specific aptamer, capable of binding to a specific ligand from a biological sample, mixing the at least one specific aptamer. The abiological sample to allow binding of the ligand to the specific one aptamer, and detecting the presence and/or quantity of the specific ligand from the biological sample bound to at least one aptamer. The captamer of the invention is useful as a drug and for therapeutic treatment. The present sequence represents a 50 bp spacer oligonucleotide used in the construction of an aptamer of the invention
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                                                                                                                   New aptamer comprising one base capable of base pairing and different from the standard Watson-Crick base, useful for isolating a specific ligand from a pool of ligands.
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Pred. No. 2.1e+04;
0; Mismatches 4; Indels
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78.9%;
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The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ003152) each having 50 base pairs (Dp). The system is useful for leukocyte expression profiling. It is particularly useful for

New system for leukocyte expression profiling, diagnosing a disease, or

Claim 1; Page 432; Opp; English.

Prentice J, Phillips J;

Phillips J;

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Gaps

0;

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for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.
diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, ridney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
                                                                                                                                                                                                                                                                                                                                                                                                      Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Constructing strains for identifying gene products as effective targets
                                                                                                                                                                                                                                                                                                                                                                               Candida gene related tetracyclin promoter PCR primer SEQ ID NO 3069
                                                                                                                                        6; Length 50;
                                                                                                                                                                    4; Indels
                                                                                                           Sequence 50 BP; 13 A; 11 C; 11 G; 15 T; 0 U; 0 Other;
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                                                                                                                                        Score 12.6; DB 6;
Pred. No. 2.1e+04;
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                                                                                                                                                                                              1 AGTAACATCTATGTTTGGT 19
                                                                                                                                                                                                                       34 AGTAACATGAATGTTGTGT 16
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                                                                                                                                                                                                                                                                                               ABZ28986 standard; DNA; 55 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-DEC-2000; 2000US-0259128P.
20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
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                                                                                                                                        63.0%;
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                                                                                                                                                     Best Local Similarity 78.9
Matches 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-566694/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Candida albicans
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                                                                                                                                                                                                                                                                                                                         ABZ28986;
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The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by complete and promoter replacement fragment with a heterologous recombination, of a promoter replacement fragment with a heterologous promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles modified are useful for identifying a gene that cells having both alleles modified are useful for identifying a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon

Claim 76; SEQ ID NO 3069; 167pp + Sequence Listing; English

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compound catabolism, biosynthetic, transporter, transcriptional, translational, signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of a PCR primer used in the method of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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Search completed: September 23, 2004, 15:59:49 Job time : 190 secs

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548, App 216, App 3, Appli 58587, A 58595, A

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58587, A 58595, A

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1712, Ap 1887, Ap 2716, Ap 25123, A 27074, A 29910, A 35597, A

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Database

us-10-798-923a-36.szlm80.rnpb

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US-09-877-478-848

US-03-42-902-145

US-10-342-902-145

US-10-669-841-848

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US-10-669-841-848

US-10-669-841-848

US-10-669-841-848

US-10-688-706-3025

US-10-688-706-3035

US-10-1215-112-6520

US-10-215-112-6520

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Sequence 2863, Ap
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Sequence 14, Appl
Sequence 3574, Ap
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Sequence 2763, Ap
Sequence 3, Appli
Sequence 27, Appl
Sequence 17106, A
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60525, A
46, Appl
                                                                                            September 23, 2004, 15:56:54; Search time 220 Seconds (without alignments) 460.450 Million cell updates/sec
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(cgn2 6/ptodata/2/pubpna/US67_PUBCOMB.seq:*

(cgn2 6/ptodata/2/pubpna/DS67_NEW_PUB.seq:*

(cgn2 6/ptodata/2/pubpna/US66_NEW_PUB.seq:*

(cgn2 6/ptodata/2/pubpna/US66_PUBCOMB.seq:*

(cgn2 6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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S US-10-099-2639-60525

S US-10-428-376-46

S US-10-428-39-5

T US-10-688-706-2763

5 US-10-043-639-3

5 US-10-098-2638-17106

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Maximum Match 100%
Listing first 150 summaries
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Perfect score:
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Sequence 36372, A Sequence 16195, A Sequence 10100, Sequence 128010, Sequence 272, Applisequence 272, Applisequence 271, Applisequence 285, Apsequence 2856, Apsequence 2717, Apsequence 10345, Apsequence 10345, Assequence 61987, Assequence 61987, Assequence 5074, Apsequence 10345, Assequence 12895, Assequence 12895, Assequence 12895, Assequence 12895, Assequence 13895, Assequence

Sequence 26, Appl Sequence 21, Appl

Sequence Sequence Sequence Sequence Sequence

11111 121110 1411111

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Result No ö

Gaps

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Indels

Length 37;

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RESULT 3
US-09-642-776A-46

19-09-642-776A-46

Sequence 46, Application US/09842776A

Publication No. US20040023316A1

GENERAL INFORMATION:
TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
TITLE OF INVENTION: IN THE STOOL
TITLE OF INVENTION: IN THE STOOL
TITLE OF INVENTION: IN THE STOOL
PILE REFERENCE: 41735

CURRENT APPLICATION NUMBER: US/09/842,776A

CURRENT APPLICATION NUMBER: PCT/EP99/08212

PRIOR FILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 64

SOFTWARE: Patentin Ver. 2.1

LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-098-263B-60525

US-10-098-263B-60525

Sequence 60525, Application US/10098263B

Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Mittman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098,263B

CURRENT APPLICATION NUMBER: 60/276,759

PRIOR PILING DATE: 2001-03-16

NUMBER: OF SEQ ID NOS: 131066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 60525

LENGTH: 255
APPLICANT: Agoston, Denes V.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCING
FILE REPERENCE: 268422000100
CURRENT PILIANG DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 60/265,113
PRIOR FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
SEG ID 
                                                                                                                                                                                                                                                                                                                Query Match 76.0%; Score 15.2; DB 15; Best Local Similarity 85.0%; Pred. No. 2.2e+03; Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.0%; Score 14.4; DB 15; 93.8%; Pred. No. 4.8e+03; ive 0; Mismatches 1;
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CORGANISM: Homo sapien
US-10-098-263B-60525
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Best Local Similarity
Matches 15; Conservat
                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Rat
US-10-059-273-6
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                        Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 11326,
Sequence 11326,
Sequence 11326,
Sequence 2172, Appl
Sequence 2172, Appl
Sequence 133, Appl
Sequence 2886, Appl
Sequence 2886, Appl
Sequence 210, Appl
Sequence 210, Appl
Sequence 520, Appl
Sequence 520, Appl
Sequence 520, Appl
Sequence 521, Appl
Sequence 520, Appl
Sequence 520, Appl
Sequence 520, Appl
Sequence 520, Appl
Sequence 1319, Appl
Sequence 226, Appl
Sequence 2313, Appl
Sequence 2313, Appl
Sequence 31622, A
Sequence 31622, A
Sequence 5172, Appl
Sequence 31622, A
Sequence 31622, A
Sequence 31622, A
Sequence 31622, A
Sequence 31626, Appl
Sequence 4982, Appl
Sequence 4982, Appl
Sequence 4982, Appl
Sequence 4982, Appl
Sequence 6137, Appl
Sequence 6137, Appl
Sequence 6137, Appl
Sequence 10839, Appl
Sequence 6137, Appl
Sequence 6137, Appl
Sequence 6137, Appl
Sequence 10839, Appl
Sequence 10830
  US-10-124-747-21
US-10-307-204-21
US-10-307-204-21
US-10-608-263B-19514
US-10-098-263B-19514
US-10-098-263B-19514
US-10-098-263B-19514
US-10-098-263B-19306
US-10-098-263B-19306
US-10-098-263B-19306
US-10-175-169-2172
US-10-175-169-2172
US-10-175-169-2172
US-10-175-169-2172
US-10-175-169-2172
US-10-175-169-2172
US-10-175-169-2172
US-10-171-1913-43
US-10-171-1913-43
US-10-171-1913-43
US-10-171-1913-69
US-10-081-263B-16287
US-10-081-263B-16287
US-10-081-263B-172-88
US-10-081-263B-172-88
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0 US-09-741-744A-146

6 US-10-339-268A-37

6 US-10-349-143-2712

5 US-10-066-544-3085

1 US-10-03-9348-3842

1 US-10-03-938-3342
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US-10-329-624-4982
US-09-908-975-6137
US-09-908-975-10839
US-09-908-975-10839
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ALIGNMENTS

US-10-059-273-6/c; Sequence 6, Application US/10059273; Publication No. US20030170736A1; GENERAL INFORMATION:

TYPE: DNA ORGANISM: Artificial Sequence

Length 20;

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Query Match
Best Local Similarity 80.05
Matches 16; Conservative
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                               Description of Artificial Sequence: DNA encoding
                         OTHER INFORMATION: Description of Artificial Sequence: DNA encoding;
CTHER INFORMATION: complementarity determining region (CDR1) of an CTHER INFORMATION: antibody light chain directed to a beta-urease;
CTHER INFORMATION: epitope (alternative sequence)
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APPLICANT: Broschat, Kay
TITLE OF INVENENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
FILE REFERENCE: 0133/1
CURRENT APPLICATION NUMBER: US/10/688,706
CURRENT APPLICATION NUMBER: 05/19,268
PRIOR APPLICATION NUMBER: 60/419,268
PRIOR APPLICATION NUMBER: 60/419,268
PRIOR FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 3071
SOFTWARE: Patentin version 3.2
IENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:

OTHER INFORMATION: Description of Artificial Sequence; note = OTHER INFORMATION: synthetic construct
US-10-428-339-5
                                                                                                                                                                                Query Match 69.0%; Score 13.8; DB 13; Length 33; Best Local Similarity 88.2%; Pred. No. 9.4e+03; Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.0%; Score 13.8; DB 16; Length 77; 88.2%; Pred. No. 1.1e+04; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-428-339-5/c

| Sequence 5, Application US/10428339 |
| Publication No. US20030228612A1 |
| APPLICANT: KENWARD, Kimberly D. |
| APPLICANT: KENWARD, Kimberly D. |
| TITLE OF INVENTION: PRODUCTION OF RECOMBINANT EPIDERMAL |
| TITLE OF INVENTION: GROWTH FACTOR IN PLANTS |
| FILE REFERENCE: 011.000504 |
| CURRENT APPLICATION NUMBER: US/10/428,339 |
| CURRENT FILING DATE: 2003-04-30 |
| PRIOR FILING DATE: 2003-04-30 |
| NUMBER OF SEQ ID NOS: 41 |
| SOFTWARE FASISEQ for Windows Version 4.0 |
| LENGTH: 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2763, Application US/10688706
Publication No. US20040102412A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  4 AACAICIAIGITIGGIT 20
                                                                                                                                                                                                                                                                                                                              13 AACATTAATGTTTGGTT 29
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.2
Matches 15; Conservative
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US-10-688-706-2763/c
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APPLICANT: SARCARAL,
APPLICANT: CRONILLY,
PATRICIA
APPLICANT: SOUCALLLE, PHILIPPE
TITLE OF INVENTION: METHOD FOR PREPARING 1,3-PROPANEDIOL BY A RECOMBINANT
TITLE OF INVENTION: MICRO-ORGANISM IN THE ABSENCE OF COENZYME B12 OR ONE OF
TITLE OF INVENTION: ITS PRECURSORS
TITLE OF INVENTION: ITS PRECURSORS
TITLE OF INTUNION: ITS PRECURSORS
FILE REFERENCE: CHEP:004US
CURRENT FILING DATE: 2003-04-12
PRIOR PLILING DATE: 2000-07-07
PRIOR PLILING DATE: 2000-07-07
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 10
SOUTHARE PRECURS PRECURSORS
SEQ ID NOS: 10
SEQ ID NO 3
LENGTH: 28
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Sequence 27, Application US/09911132A

Publication No. US20030096341A1

GENERAL INFORMATION:
APPLICANT: Roche Diagnostics GmbH

TITLE OF INVENTION: Expression of Alkaline Phosphatase in Yeast
FILE REFERENCE: RDD 0073US

CURRENT APPLICATION NUMBER: US/09/911,132A

CURRENT FILING DATE: 2002-08-28

NUMBER OF SEO ID NOS: 38

SOFTWARE: PatentIn version 3.1

SEQ ID NO 27

LENGTH: 73
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Score 13.6; DB 17;
Pred. No. 1.1e+04;
0; Mismatches 4;
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Pred. No. 1.1e+04;
0; Mismatches 4;
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Best Local Similarity 80.0%; Pred. No. 1.3e+04;
Matches 16; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                            Sequence 3, Application US/10043639A Publication No. US20030175916A1 GENERAL INFORMATION:
                                                                                                 1 AGTAACATCTATGTTTGGTT 20
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                                                                                                                                          20 ATTTATATCTAAGTTTGGTT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Clostridium butyricum
    68.0%;
80.0%;
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Best Local Similarity 80.0%;
Matches 16; Conservative
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| Sequence 2866, Application US/10688706
| Sublication No. US20040102412A1
| GENERAL INFORMATION:
| APPLICANT: Pharmacia Corp. |
| APPLICANT: Broachat, Kay
| TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
| FILE REPERENCE: 01393/1 |
| CURRENT FILING DATE: 2003-10-17 |
| CURRENT FILING DATE: 2003-10-17 |
| NUMBER OF SEQ ID NOS: 3071 |
| SOFTWARE: Patentin version 3.2 |
| SEQ ID NO 2868 |
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 66.0%; Score 13.2; DB 17; Length 20; Best Local Similarity 83.3%; Pred. No. 1.7e+04; Matches 15; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE COMPUTER: 1BM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.0%; Score 13.2; DB 17;
83.3%; Pred. No. 1.7e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: human GFAT antisense US-10-688-706-2868
                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: human GFAT antisense US-10-688-706-2863
PRIOR APPLICATION NUMBER: 60/419,268
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Patent No. US20020102550A1
GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: AMSTER, ROTHS'
STREET: 90 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10016
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                           PRIOR FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 3071
SOFTWARE: Patentin version 3.2
SEQ ID NO 2863
LENGTH: 20
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                                                                                                                                                                                           TYPE: DNA ORGANISM: artificial
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US-10-688-706-2868/c
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US-09-753-143-14
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; Sequence 3917, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52579)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR PELING DATE: 2001-01-05
; PRIOR PELING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR APPLICATION NUMBER: US 09/855,768
; RING DATE: 2001-01-13
; PRIOR PILING DATE: 2001-01-15
; NUMBER OF SEQ ID NOS: 4593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 25;
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                                                                                                                                                     APPLICATION MICHAEL
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 31181
FILE REFERENCE: 31181
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 17106
LENGTH: 25
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APPLICANT: Broschat, Kay
TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
FILE REFERENCE: 01393/11
CURRENT APPLICATION NUMBER: US/10/688,706
CURRENT FILING DATE: 2003-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Pred. No. 1.4e+04;
0; Mismatches 1;
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Pred. No. 1.7e+04;
0; Mismatches 3;
                                                             Sequence 17106, Application US/10098263B Publication No. US20030104410A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2863, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
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83.3%;
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Best Local Similarity 83...
Best Local Similarity
The state of the stat
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Best Local Similarity 93.33
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-17106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Glycine max US-09-969-373-3917
                              US-10-098-263B-17106/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-969-373-3917/c
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LENGTH: 20
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Gaps

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US-09-877-478-148-148

US-09-877-478-148-148

Sequence 145, Application US/09877478

Publication No. UB20030068301A1

GENERAL INFORMATION:

APPLICANT: Elback, Kenneth

APPLICANT: Blatt, Larry

APPLICANT: McSwiggen, Jim

FRIOR PLIANG DATE: 1992-06-14

PRIOR APPLICATION NUMBER: US 09/636,385

PRIOR APPLICATION NUMBER: US 09/636,347

PRIOR APPLICATION NUMBER: US 09/636,347

PRIOR APPLICATION NUMBER: US 08/433,504

PRIOR PLIANG DATE: 1994-02-07

PRIOR PLIANG DATE: 1995-05-04

PRIOR APPLICATION NUMBER: US 08/433,504

PRIOR PLIANG DATE: 1995-05-04

PRIOR APPLICATION NUMBER: US 08/434,504

PRIOR APPLICATION NUMBER: US 08/434,504
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; Sequence 848, Application US/09877478
; Sequence 848, Application US/09877478
; Publication No. US2003068301A1
; GENERAL INFORMATION:
    APPLICANT: Ribozyme Pharmaceuticals, Inc.
    APPLICANT: Draper, Kenneth
    APPLICANT: Draper, Kenneth
    APPLICANT: Mcwiggen, Jim
    FILE REFERENCE: MeHB00-845-H (400/029)
; CURRENT FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,347
; PRIOR FILING DATE: 2000-08-09
; PRIOR FILING DATE: 1994-02-07
; PRIOR FILING DATE: 1994-02-07
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR APPLICATION NUMBER: US 08/433,993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGTAACATCTATGTTT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Hepatitis B virus US-09-877-478-145
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US-10-032-585-3574
US-10-032-585-3574
Sequence 3574, Application US/10032585
Publication No. US20030180953A1
GENERAL INFORMATION:
APPLICANT: Terry, Koemer D.
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
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                    CURRENT APPLICATION DATA:
AND LICATION DATA:
APPLICATION NUMBER: US/09/753,143
FILING DATE: 02-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/175,828
FILING DATE: 1998-10-20
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 63475/65
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 86-0854 OI 286-0082
TELEFAX: (212) 286-0854 OI 286-0082
TELEFAX: (212) 286-0854 OI 286-0082
TELEX: TWX 710-581-4766
INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: «UNKNOWN»
DESCRIPTION: OTHER NUCLEIC ACID
MAND OFFICEL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTIFICATION METHOD:
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Best Local Similarity 83.3%;
Matches 15; Conservative
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US-10-032-585-3574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO FEATURE:
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LENGTH: 65
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APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Stram Therapeutics, Inc.
APPLICANT: Lawrence, Blatt
APPLICANT: Demnis, Macejak
APPLICANT: Demnis, Macejak
APPLICANT: David, Morrissey
APPLICANT: David, Morrissey
APPLICANT: David, Morrissey
APPLICANT: Pamela, Pavoo
APPLICANT: Pamela, Pavoo
APPLICANT: Pamela, Pavoo
APPLICANT: Renneth, Draper
APPLICANT: Wenter Renneth, Draper
APPLICANT: Wenter Renneth, Use APPLICANTON: VIRUS REPLICANTON
TITLE OF INVENTION: VIRUS REPLICANTON
TITLE OF INVENTION NUMBER: US 60/335,059
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-02-2
PRIOR APPLICANTON NUMBER: US 60/337,055
PRIOR FILING DATE: 2001-02-2
PRIOR FILING DATE: 2002-03-11
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2000-03-26
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2000-03-26
PRIOR FILING DATE: 2000-12-18
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50.0%; Pred. No. 2.5e+04;
"":matches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 145, Application US/10669841; Publication No. US20040127446A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-10-342-902-848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 50.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SILING Inergettics, inc.
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Mcswiggen, Jim
APPLICANT: Mcswiggen, Jim
APPLICANT: Mcswiggen, Jim
APPLICANT: Mcswiggen, Jim
APPLICANT: Mcsrissey, Dave
ITILE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: 4000/075 (MHBBO-845-I)
CURRENT PILING DATE: 2003-01-15
FRIOR FILING DATE: 2001-06-08
FRIOR FILING DATE: 2001-06-08
FRIOR FILING DATE: 2000-03-20
FRIOR FILING DATE: 2000-03-20
FRIOR FILING DATE: 2000-01-024
FRIOR FILING DATE: 2000-01-024
FRIOR FILING DATE: 1994-02-07
FRIOR FILING DATE: 1994-02-07
FRIOR FILING DATE: 1994-02-07
FRIOR FILING DATE: 1994-02-07
FRIOR FILING DATE: 1992-06-14
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Pred. No. 2.5e+04;
6; Mismatches 2; Indels
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Pred. No. 2.5e+04;
5; Mismatches 2; Indels (
PRIOR APPLICATION NUMBER: US 08/434,504
PRIOR FILING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6586
SOFTWARE: Patentin version 3.0
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Publication No. US20040054156A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Draper, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 145, Application US/10342902
Publication No. US20040054156A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
                                                                                                                                                                                                                                                                                         Similarity 50.0%; 8; Conservative (
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 145
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Best Local Similarity 50.0%;
Matches 8; Conservative (
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                                                                                                                                                                                                                 ; ORGANISM: Hepatitis B virus US-09-877-478-848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: RNA
ORGANISM: Hepatitis B virus
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                   Sequence 3025, Application US/10688706
; Sequence 3025, Application US/10688706
; Publication No. US2040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REPERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SEQ ID NO 3025
; LENGTH: 20
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Publication No. US20040102412A1
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Broschat, Kay
TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
FILE REFERENCE: 01393/1
CURRENT APPLICATION NUMBER: US/10/688,706
CURRENT FILING DATE: 2003-10-17
PRIOR FILING DATE: 2002-10-17
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Best Local Similarity 87.5%; Pred. No. 2.5e+04;
Matches 14; Conservative 0; Mismatches 2;
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US-10-215-112-6520
; Sequence 6520, Application US/10215112
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SEQ ID NO 3034
LENGTH: 20
                                       2 AGGAACCUCUAUGUUU 17
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PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR PLING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/504,321
PRIOR FILING DATE: 2000-02-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEC ID NOS: 16207
SOFTWARE: PatentIn version 3:0
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Publication No. US20040127446A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sirna Therapeutics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 64.0%;
Best Local Similarity 50.0%;
Matches 8; Conservative
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Dennis, Macejak
James, McSwiggen
David, Morrissey
                                                                                                                                                                         ; ORGANISM: Hepatitis B Virus US-10-669-841-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Hepatitis B Virus US-10-669-841-848
                                                                                                                                                          TYPE: RNA
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CURRENT APPLICATION NUMBER: US/10/099,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                      Sequence 60526, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
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Publication No. US20040175743A1
GENERAL INFORMATION:
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                                                                                                                                              4 AACATCTATGTTTGGT 19
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Best Local Similarity 97.5
Matches 14, Conservative
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; ORGANISM: Homo sapien
US-10-098-263B-60526
               ; ORGANISM: Homo sapien
US-10-098-263B-1523
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US-10-098-263B-60526
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; ORGANISM: probe
US-10-775-169-3303
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Matches 14;
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| Publication No. US20030082596A1
| GENERAL INFORMATION:
| APPLICANT: Michael Mittmann
| TITLE OF INVENTION: Test3
| FILE REFERENCE: 3119
| CURRENT APPLICATION NUMBER: US/10/215,112
| CURRENT FILING DATE: 2002-08-08
| NUMBER OF SEQ ID NOS: 14936
| SOFTWARE FREESEQ FOR Windows Version 4.0
                              APPLICANT: Michael Mittmann
TITLE OF INVENTION: Method of Genetic Analysis of Probes:
TITLE OF INVENTION: Test3
TITLE OF INVENTION: Test3
FILE REFERENCE: 3119
CURRENT APPLICATION NUMBER: US/10/215,112
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 14936
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 6220
LENGTH: 25
                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Synthetic Oligonucleotide US-10-215-112-6520
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; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-10981
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Publication No. US20030082596A1
                   GENERAL INFORMATION:
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US-10-098-263B-1523
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LENGTH: 25
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APPLICANT: Bucczynski, Michael
APPLICANT: Twine, Nachale
APPLICANT: Treine, Nachael
APPLICANT: Treine, Nathew
APPLICANT: Treine Cocho, William
APPLICANTON: Method for Monitoring Drug Activities In Vivo
FILE REFERENCE: AM101080 (031896-013000)
CURRENT FILING DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 5278
SGPTWARE: PatentIn version 3.2
LENGTH: 25
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SOTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 60526
LENGTH: 25
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87.5%; Pred. No. 2.6e+04;
live 0; Mismatches 2;
Query Match 64.0%; Score 12.8; DB 15; Best Local Similarity 87.5%; Pred. No. 2.6e+04; Matches 14; Conservative 0; Mismatches 2;
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OTHER INFORMATION: Primer US-10-168-445-216
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US-10-027-632-58587/c
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US-10-022-623-548
US-10-026-623-548

US-10-026-623-548

Sequence 548, Application US/10002623

Publication No. US2003013428541

GENERAL INFORMATION:
APPLICANT: UNDERHILL, PETER A.
TITLE OF INVENTION: A METHOD FOR DETERMINING GENETIC
TITLE OF INVENTION: A PFILLATION, SUBSTRUCTURE AND GENE FLOW WITHIN HUMAN
TITLE OF INVENTION: A PFILLATION'S FILE AT STATE OF INVENTION: APPLICATION NUMBER: US/10/002,623

CURRENT APPLICATION NUMBER: US 60/245,355

PRIOR PELLING DATE: 2000-11-01

NUMBER OF SEQ ID NOS: 952

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 548

LENGTH: 27
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APPLICANT: Twine, Natalie
APPLICANT: Dorner, Andrew
APPLICANT: Dorner, Andrew
APPLICANT: Trepicchio, William
APPLICANT: Trepicchio, William
APPLICANT: Trepicchio, William
APPLICANT: TILLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
FILE REFERENCE: AMMONGEN: US/10/775,169
CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT FILING DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 5278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3304
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 25;
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Best Local Similarity 87.5%; Pred. No. 2.6e+04;
Matches 14; Conservative 0; Mismatches 2;
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US-10-775-169-3304/c
; Sequence 3304, Application US/10775169
; Publication No. US20040175743A1
; GRNERAL INFORMATION:
; APPLICANT: Wyeth
                                                                                                                        Burczynski, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: probe
US-10-775-169-3304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-002-623-548
                                                                                                                        APPLICANT:
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Sequence 3, Application US/10353274

Sequence 3, Application WS/258991

Sequence 3, Application WS/258991

Fublication No. US20302358991

GENERAL INFORMATION:
TITLE OF INVENTION: CATALYTIC DOMAIN OF THE HUMAN EFFECTOR CELL CYCLE CHECKPOINT PROT

TITLE OF INVENTION: CATALYTIC DOMAIN OF THE HUMAN EFFECTOR CELL CYCLE CHECKPOINT PROT

TITLE OF INVENTION: CATALYTIC DOMAIN OF THE HUMAN EFFECTOR CELL CYCLE CHECKPOINT PROT

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TITLE OF INVENTION: CATALYTIC DOMAIN OF THE HUMAN EFFECTOR CELL CYCLE CHECKPOINT PROT

TITLE OF INVENTION: CATALYTIC DOMAIN OF THE HUMAN EFFECTOR CELL CYCLE CHECKPOINT PROT

TITLE OF INVENTION: CATALYTIC DOMAIN OF THE HUMAN EFFECTOR CELL CYCLE CHECKPOINT PROT

TITLE OF INVENTION OF THE HUMAN EFFECTOR CELL CYCLE CHECKPOINT PROT

TITLE OF INVENTION OF THE HUMAN EFFECTOR CELL CYCLE CHECKPOINT PROT

TITLE OF INVENTION OF THE HUMAN EFFECTOR CHECKPOINT PROT

TITLE OF INVENTION OF THE HUMAN EFFECTOR CHECKPOINT PROT

TITLE OF INVENTION OF THE HUMAN EFFECTOR CHECKPOINT PROT

TITLE OFF
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Publication No. US2020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION POLYMORPHISMS in the Human Genome
TITLE OF INVENTION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
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CURRENT APPLICATION NUMBER: US/10/168,445
CURRENT FILING DATE: 2002-10-30
PRIOR APPLICATION UNBER: PCT/GB00/04908
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 1999-12-22
PRIOR RILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: GB 0020217.6
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 219
SOFTWARE: PatentIn version 3.0
SOFTWARE: PatentIn version 3.0
LENGTH: 30
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SOFTWARE: Patentin version 3.1
SEQ ID NO 34
LENGTH: 34
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GENERAL INCURANTION:

JAPPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
FRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-07-20
PRIOR PLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PLING DATE: 2000-05-24
PRIOR PLING DATE: 12000-05-24
PRIOR PLING DATE: 1990-09-28
PRIOR PLING DATE: 1990-09-28
PRIOR PLING DATE: 1990-09-28
PRIOR FILING DATE: 1990-09-28
PRIOR FILING DATE: 1990-09-08
PRIOR FILING DATE: 1990-09-08
PRIOR FILING DATE: 1990-09-08
PRIOR FILING DATE: 1990-08-08
PRIOR FILING DATE: PAREAGE for Windows Version 4.0
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 10827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT PILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR APPLICATION NUMBER: US 60/165,358
PRIOR FILING DATE: 1909-09-28
PRIOR FILING DATE: 1999-09-28
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Pred. No. 2.8e+04;
1. Mismatches 3;
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; Sequence 58595, Application US/10027632
; Publication No. US20030204075A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19
                Publication No. US20030204075A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.8%;
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Best Local Similarity
Matches 14; Conserv
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; ORGANISM: Human
US-10-027-632-58587
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SEQ ID NO 58595
LENGTH: 36
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Pred. No. 2.8e+04;
1; Mismatches 3; Indels
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Pred. No. 2.8e+04;
L; Mismatches 3; Indels
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-08-28
PRIOR FILING DATE: 1999-08-28
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SEQ ID NO 58587
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US-10-027-632-58587/c
; Sequence 58587, Application US/10027632
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77.8%;
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Best Local Similarity 77.8%;
Matches 14; Conservative
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Best Local Similarity 77.8'
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58587
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US-10-027-632-58595
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Publication No. US20040102412A1

GENERAL INFORMATION:

APPLICANT: Pharmacia Corp.

APPLICANT: PRASTION: ANTISENSE MODULATION OF GFAT EXPRESSION

TILLE REFERENCE: 01393/1

CURRENT APPLICATION NUMBER: US/10/688,706

CURRENT FILING DATE: 2003-10-17

PRIOR APPLICATION NUMBER: 60/419,268

PRIOR FILING DATE: 2002-10-17

SOFTWARE: PALENTIN VERSION 3.2

SEQ ID NO 2716

LENGTH: 20
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Sequence 25123, Application US/10098263B

Publication No. US20030104410A1

GENERAL INFORMATION:

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098,263B

CURRENT FILING DATE: 2003-01-08

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 131066

SOFFWARE: Microarray Probe Sequence Listing Generator V 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.0%; Score 12.6; DB 17; 78.9%; Pred. No. 3.1e+04; cive 0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: human GFAT antisense US-10-688-706-2716
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TITLE OF INVENTION: Human Microarray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AGTAACATCTATGTTTGGT 19
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                                        43 ACATTTATGTTTGTTT 28
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Best Local Similarity 78.9
Matches 15; Conservative
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Best Local Similarity 78.9
Matches 15; Conservative
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CORGANISM: Homo sapien
US-10-098-263B-25123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: artificial
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US-10-098-263B-27074
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LENGTH: 25
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Sequence 1887, Application US/10349143

Publication No. US20040005584A1

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Cohen, Daniel

APPLICANT: Chumakov, Ilya

TITLE OF INVENTION Biallelic markers for use in constructing a high density...

FILE REFERENCE: GENSET. 02002D1

CURRENT APPLICATION NUMBER: US/10/349,143

CURRENT APPLICATION NUMBER: US/09/422,978

PRIOR PILING DATE: EARLIER FILING DATE: 1999-10-20

PRIOR PILING DATE: EARLIER FILING DATE: 1999-04-21

PRIOR PELING DATE: EARLIER FILING DATE: 1998-11-23

PRIOR PELING DATE: EARLIER FILING DATE: 1998-11-23

**PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

**SEQ ID NOS: 11796

**SEX ID NO 1887
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                                                                                                                                                                                                                                                                                           APPLICANT: Terry, Roemer D.
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Bo, Jiang
APPLICANT: Bo, Jiang
APPLICANT: Bo, Jiang
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
LENGTH: 43
                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.0%; Score 12.8; DB 15; Length 43; 87.5%; Pred. No. 2.9e+04;
Pred. No. 2.8e+04;
1; Mismatches 3; Indels
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; OTHER INFORMATION: 99-7129-335 : polymorphic base A or C
US-10-349-143-1887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                          ; Sequence 1712, Application US/10032585; Publication No. US20030180953A1; GENERAL INFORMATION:
                                                                   2 GTAACATCTAIGTTIGGT 19
                                                                                                18 GGAACTTCYGTGTTTGGT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 AGATCTATGTTTGTTT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 ACATCTATGTTTGGTT 20
Best Local Similarity 77.8%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Candida albicans
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Best Local Similarity 87.5
Matches 14; Conservative
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                          US-10-032-585-1712/c
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US-10-349-143-1887/c
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US-10-098-263B-35736/c
US-10-098-263B-35736, Application US/10098263B
Sequence 35736, Application US/10098263B
Publication No. US20030104410A1
SERVERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR APPLICATION NUMBER: 60/276,759
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
TOWNSHIP OF SEQ ID NOS: 131066
SEQ ID NO 35736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-098-263B-36372/C

Sequence 36372, Application US/10098263B

Publication No. US2030104410A1

GENERAL INFORMATION:

APPLICANT: Mittman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT FILING DATE: 2003-01-08

PRIOR PILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 131066

SOFTWARRE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 36372

LENGTH: 25
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      Indels
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        0; Mismatches
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; Sequence 65195, Application US/10098263B;
; Publication No. US20030104410A1
; GENERAL INFORMATION:
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TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
                                               2 GTAACATCTATGTTTGGTT 20
                                                                                    1 Gradcaggradgrircgri 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGTAACATCTATGTTTGGT 19
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      15; Conservative
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Best Local Similarity 78.9
Matches 15, Conservative
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CORGANISM: Homo sapien
US-10-098-263B-36372
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Matches 15; Conserv
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        Matches
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APPLICANT: Mittman, Michael

TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098,263B

CURRENT PILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: 60/276,759

PRIOR APPLICATION NUMBER: 60/276,759

PRIOR APPLICATION NUMBER: 001-03-16

NUMBER OF SEQ ID NOS: 131066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mittenan, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT FILING DATE: 2003-01-08
FRIOR APPLICATION NUMBER: 60/276,759
FRIOR FILING DATE: 2001-0.08
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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Pred. No. 3.2e+04;
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                                                                                                                                                                                                                                                                               Length 25;
FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098,263B

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: 60/276,759

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 131066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 27074

LENGTH: 25
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Pred. No. 3.2e+04;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 29910, Application US/10098263B Publication No. US20030104410A1
                                                                                                                                                                                                                                                                                                                                                             1 AGTAACATCTATGTTTGGT 19
                                                                                                                                                                                                                                                                                                                                                                                           1 AGTAATAGATATGTTTCGT 19
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78.9%;
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Best Local Similarity 78.9<sup>3</sup>
Matches 15; Conservative
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Matches 15; Conservative
                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapien
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; ORGANISM: Homo sapien
US-10-098-263B-35597
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Best Local Similarity
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US-10-098-263B-29910/c
                                                                                                                                                                                                                      ; UKGAN13M: DUMU US-10-098-263B-27074
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                                                                                                                                                                           Query Match 63.0%; Score 12.6; DB 15; Length 25; Best Local Similarity 78.9%; Pred. No. 3.2e+04; Matches 15; Conservative 0; Mismatches 4; Indels C
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION UMBER: e0/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: M.Croarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 61195
LENGTH: 25
                                                                                                                                                                                                                                      2 GTAACATCTATGTTTGGTT 20
                                                                                                                                                                                                                                                           2 GTAACAGGTAGGTTTCGTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapien
US-10-098-263B-100102
                                                                                                                       TYPE: DNA
CORGANISM: Homo sapien
US-10-098-263B-65195
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52, Appl
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1887, Ap
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5, Appli
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198, App
199, App
                             9; Search time 53 Seconds
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209.415 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
  GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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S-08-956-171E-4982
S-08-303-275-198
S-08-303-275-199
                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                               682709 seqs, 277475446 residues
                             September 23, 2004, 15:45:09
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Maximum Match 100%
Listing first 150 summaries
                   OM nucleic - nucleic search, using sw model
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VGC-US95-077444-57
US-09-287-796-149
US-09-130-616-149
US-09-130-616-149
US-08-320-373-1
US-08-320-373-1
US-08-956-171E-2061
US-08-956-171E-4977
US-09-96-171E-4977
US-09-96-171E-5031
US-09-462-941-29
US-08-398-617-6
US-08-398-617-6
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US-08-398-617-6
US-08-398-615-6
US-08-398-615-6 US-08-398-615-4 US-08-399-615-4 US-08-398-6171E-4957 US-08-398-617-18 US-08-398-617-18 US-08-398-617-19 US-08-398-617-20 US-08-398-617-20 US-08-397-303-12 US-09-387-341-221 US-09-088-361-22 US-09-088-361-22 US-09-253-025-20 US-09-253-025-20 US-09-59-48B-2 US-09-59-48B-2 US-08-50-125-15 US-08-10-125-15 US-08-10-125-15 US-08-10-125-15 US-08-10-125-15 US-08-10-125-15 US-08-10-125-10 PCT-US93-04717-27 US-09-786-569-8 US-09-786-569-9 US-08-398-617-4 US-08-398-617-22 US-08-398-615-16 US-08-397-303-21 US-08-397-303-22 -08-398-617-11 -08-398-617-12 US-08-398-615-11 US-08-398-615-12 US-08-397-303-11 US-08-398-615-22 US-08-397-303-16 US-08-397-303-18 US-08-398-615-21 US-08-398-61 US-08-398-61 US-08-398-61

US-07-936-533A-6

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APPLICANT: Croteau, Rodney B
APPLICANT: Croteau, Rodney B
APPLICANT: Hefner, Jerry
TITLE OF INVENTION: Synthage, And Methods of Use
FILE REFERENCE: WSUR12423
CURRENT APPLICATION UNMBER: US/09/187,050B
CURRENT FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN Ver. 2.0
                                                                                Gaps
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LOCATION: (1)...(43)
LOCHER INPORMATION: PCR primer for synthesizing Tr295 truncation
OTHER INFORMATION: product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 43;
                                                 Score 13.8; DB 3; Length 2 Pred. No. 5.3e+02; O; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/08559303B
Patent No. 5824501
GENERAL INFORMATION:
APPLICANT: NATHAN A. ELLIS, JAMES GERMAN, AND JOANNA APPLICANT: GROBEN
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: OF BLOOM'S SYNDROME
NUMBER OF SEQUENCES:
ADDRESSEE: AMSTER, ROTHSTEIN & BEENSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.0%; Score 13.8; DB 3;
88.2%; Pred. No. 5.6e+02;
ive 0; Mismatches 2;
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-359-757-34
                                                                                                                                                                                       RESULT 2
US-09-187-050-9
Sequence 9, Application US/09187050B
Patent No. 6043072
GENERAL INFORMATION:
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                                                                                                            1 AGTAACATCTATGTTTG 17
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...: AMSTER, ROTHL.

...TY: 90 PARK AVENUE
CITY: NEW YORK
COUMTRY: U.S.A.
ZIP: 10016
MPUTER REPERENTION
                                                                                                                                          2 AGTAACATCTGTCTTTG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                    69.0%;
88.2%;
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Best Local Similarity 88.2
Matches 15, Conservative
                                                                                   Conservative
                                                    Query Match
Best Local Similarity
Matches 15; Conserv
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US-08-559-303B-14
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                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 43
                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 9
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                                                      Sequence 862, App
Sequence 18, Appl
Sequence 19, Appl
Sequence 49, Appl
Sequence 1110, Ap
Sequence 1111, Ap
Sequence 1113, Ap
Sequence 1152, Ap
Sequence 1152, Ap
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Sequence 10512, A
Sequence 44, Appl
Sequence 47, Appl
Sequence 126, App
Sequence 120, App
Sequence 1200, App
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Sequence 134, App
Sequence 4342, Ap
Sequence 20, Appl
Sequence 110, App
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Sequence 416, App
Sequence 33, Appl
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Appli
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Sequence 133, App
Sequence 134, App
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Sequence 37,
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Sequence 3
Sequence 3
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Sequence
                                                                                                    Patent No.
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                                         Sequence
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i Sequence 34, Application US/09359757

j Patent No. 6080546

j GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Brett P. Monia

APPLICANT: Lex M. Cowsert

TITLE OF INVENTION: ANTISENSE MODULATION OF MEKK5 EXPRESSION

TITLE OF INVENTION: ANTISENSE WOOULATION OF MEKK5 EXPRESSION

CURRENT APPLICATION NUMBER: US/09/359,757

CURRENT FILING DATE: 1999-07-23

NUMBER OF SEQ ID NOS: 47

LENGTH: 20
          US-07-936-533A-34
US-08-422-978-86-08-08-422-978-86-08-434-099A-18
US-08-422-978-86-18
US-08-434-099A-18
US-08-434-099A-18
US-08-434-099A-18
US-08-434-099A-18
US-08-428-082B-1110
US-09-428-082B-11110
US-09-428-082B-11113
US-08-428-082B-11113
US-08-438-082B-11113
US-08-438-082B-11113
US-08-438-082B-11113
US-08-438-082B-1113
US-09-428-082B-1113
US-09-428-082B-1113
US-09-371-772B-134
US-09-371-772B-134
US-09-428-978-10512
US-08-435-628-1152
US-08-422-978-10512
US-08-422-978-10512
US-09-422-978-10512
US-09-428-1132
US-09-55-588-68-6
US-09-973-55-125
US-08-621-897-7
US-08-98-98-75-17
US-09-38-0-255-7
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,303B
FILING DATE: NOVEMBER 15, 1995

TYPE: DNA ORGANISM: Artificial Sequence FEATURE:

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Gaps

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APPLICANT: Margosiak, Steve
APPLICANT: Margosiak, Steve
APPLICANT: Nguyen, Binh
APPLICANT: O'Connor, Batrick
APPLICANT: Register, James
APPLICANT: Russell, Anna Tempczyk
APPLICANT: Sarup, Jay
TITLE OF INVENTION: Catalytic Domain of the Human Effector Cell cycle
TITLE OF INVENTION: Checkpoint Protein Kinase, Chkl, Materials and
TITLE OF INVENTION: Checkpoint Protein Kinase, Chkl, Materials and
TITLE OF INVENTION: Methods for Identification of Inhibitors Thereof
CURRENT APPLICATION NUMBER: US/09/460,421
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 24
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; OTHER INFORMATION: Description of Artificial Sequence: PCR primer US-09-460-421-3
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Pred. No. 1e+03;
0; Mismatches 3; Indels
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64.0%; Score 12.8; DB 4;
Best Local Similarity 87.5%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 2;
       STANDED SESSIONER
STRANDED SESSIONER
TOPOLOGY: LINEAR
MOLECULE TYPE:
DESCRIPTION: OTHER NUCLEIC ACID
HYPOTHETICAL: YES
ANTI-SENSE: NO
FEATURE:
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GENERAL INFORMATION: APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09460421
Patent No. 6670167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AGTAACATCTATGTTTGG 18
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Best Local Similarity 83.3%;
Matches 15; Conservative (
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Anderson, Mark
Deng, Ya-Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AGTAACATCTATGTTT
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Kan, Chen Chen
Luo, Chun
                                                                                                                                                                                                                                 LOCATION:
1 IDENTIFICATION METHOD:
1 OTHER INFORMATION:
US-09-175-828-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                           NAME/KEY:
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SEQ ID NO 3
LENGTH: 34
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| Patent No. 6221643
| GENERAL INFORMATION |
| APPLICANT: MATHAN A. ELLIS, JAMES GERMAN, AND JOANNA APPLICANT: GRODEN
| TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT TITLE OF INVENTION: OF BLOOM'S SYNDROME NUMBER OF SEQUENCES: 78
| CORRESPONDENCE ADDRESS: ADDRESSE: MEN YORK STATE: NEW PC COMPATIBLE COMPUTER: 1BM PC COMPATIBLE COMPUTER: 1BM PC COMPATIBLE COMPATIBLE COMPUTER: 1BM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METHODS FOR DIAGNOSIS AND TREATMENT OF BLOOM'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                  | NAME: ELIZABETH A. BOGOSIAN | REGISTRATION NUMBER: 39,911 | REFERENCE/DOCKET NUMBER: 39,911 | REFERENCE/DOCKET NUMBER: 63475/65 | TELECOMUNICATION INFORMATION: TELEPHONE: (212) 697-5995 | TELEPA: (212) 286-0854 or 286-0082 | TELEX: TWX 710-581-4766 | INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/559,303
FILING DATE: NOVEMBER 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGGOSIAN
REGISTRATION NUMBER: 39,911
REPERENCE/DOCKET NUMBER: 63475/65
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWA.710-581-4766
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/175,828
                                                                                                                                                                                                                                                                                                                                                                                  OTHER NUCLEIC ACID
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MS-DOS
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Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFICATION METHOD:
COTHER INFORMATION:
US-08-559-3038-14
                                                                                                                                                                                                                                                                                                        SINGLE
                                                                                                                                                                                                                                                                      TYPE: NUCLEIC ACID
STRANDEDNESS: SINGI
TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: )
                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
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US-09-175-828-14
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Gaps

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63.0%; Score 12.6; DB 3; Length 24; 78.9%; Pred. No. 2e+03; ive 0; Mismatches 4; Indels
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TITLE OF INVENTION: No. 6348342el Compounds
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSES: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: PSEUSEQ. For Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/757,014
                     STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre CITY: Philadelphia
                                                               STATE: FILINGULPHIA
STATE: PARTIES FAND COUNTRY: USA
COUNTRY: USA
ZIP: 19103-2793
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIABLE
OFFRATING SYSTEM: Windows
SOFTWARE: FRANCSOF for Windows
SOFTWARE: FRANCSOF for Windows
SOFTWARE: TRACTION DATA:
APPLICATION NUMBER: US/08/868,699A
FILING DATE: 04-UTW-1997
CLASSIFTCATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION NUMBER:
ATTORNEY, AGENT INFORMATION:
NAME: FAIK, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: 36,795
TELESPHONE: 215-994-2488
TELESPHONE: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 09-Jan-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/868,699
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
  ADDRESSEE: Dechert, Price & Rhoads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULY >
US-09-757-014-5/c
US-09-757-014-5/c
; Sequence 5, Application US/09757014
; Patent No. 6348342
; GENERAL INFORMATION:
; APPLICANT: O'DWYER, Karen
; PELY, Caroline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GTAACATCTATGTTTGGTT 20
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SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
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Best Local Similarity 78.9
Matches 15; Conservative
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APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILTE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET. 020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-01-23
EARLIER FILING DATE: 1998-01-23
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 1887
LENGTH: 47
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APPLICANT: RODERTS, Christopher J.
TITLE OF INVENTION: ESSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNGAL
TITLE OF INVENTION: DRUGS
TITLE OF INVENTION: DRUGS
FILE REFERENCE: 9301-048
CURRENT APPLICATION NUMBER: US/09/315,793
CURRENT FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 64.0%; Score 12.8; DB 4; Length 47; Best Local Similarity 87.5%; Pred. No. 1.7e+03; Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 64.0%; Score 12.8; DB 3; Length 7. Best Local Similarity 87.5%; Pred. No. 1.8e+03; Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: allele
CCATION: 24
COTHER INFORMATION: 99-7129-335 : polymorphic base A or C
US-09-422-978-1887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08868699A
Patent No. 6204019
GENERAL INFORMATION:
APPLICANT: O'DWyer, Karen
APPLICANT: Perry, Caroline
APPLICANT: Warren, Richard L.
TITLE OF INVENTION: No. 6204019e1 Compounds
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-315-793-53/c
; Sequence 53, Application US/09315793
; Patent No. 6221597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 ACATCTATGTTTGGTT 20
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                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-868-699A-5/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDLIM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: TASKEG for Windows Version 2.0
SUFFWARE: FASTERS TOS NOTE:
SOFTWARE: 21-JAN-1998
CLASSIFICATION INTERES: US/09/009,913
FILING DATE: 21-JAN-1998
CLASSIFICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: CASAGORA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-09-009-913-223/c
; Sequence 223, Application US/09009913
; Patent No. 6087488
; GENERAL INFORMATION:
; APPLICANT: AxyS Pharmaceuticals, Inc.
; TITLE OF INVENTION: Asthma Related Genes
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM10012
REFERENCE/DOCKET NUMBER: GM10012
TELEFRONE: 215-994-222
TELEFRONE: 215-994-222
TELEFRONE: C15-994-222
                                                                                                                                                                                                                                                                                TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GTAACATCTATGTTTGGTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: SE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 GTAACATCTAGTTTATGTT
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Best Local Similarity 78.99
Matches 15; Conservative
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LENGTH: 27 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650-327-3231
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Best Local Similarity
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Sequence 3, Application US/07749446

Patent No. 5593857

GENERAL INFORMATION:
APPLICANT: Highari, Jeffrey N.
APPLICANT: Tischer, Edmund G.
APPLICANT: Cordell, Barbara
APPLICANT: Cordell, Barbara
APPLICANT: Cordell, Barbara
TITLE OF INVENTION: REDUCTION OF HOMOGENEOUS CILIARY
TITLE OF INVENTION: NEUROTROPHIC FACTOR
CORRESPONDENCE ADDRESS:
ADDRESSEE: California Biotechnology Inc.
STREET: 2450 Bayshore Parkway
CITY: Mountain View
STARET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/749,446
FILING DATE: 19911008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ballance, David J
APPLICANT: Courtney, Michael G
APPLICANT: Finnis, Christopher J A
APPLICANT: Sleep, Darrell
TITLE OF INVENTION: Medicine
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Centeon L.L.C.
STREST: 1020 First Avenue
CITY: King of Prussia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-584-760A-50
; Sequence 50, Application US/08584760A
; Patent No. 6290953
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Shearer, Peter R.
REGISTRATION NUMBER: 28,117
REFERENCE/DOCKET NUMBER: PC43:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-962-5860
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GTAACATCTATGTTTGGTT 20
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78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 63.0
Best Local Similarity 78.9
Matches 15, Conservative
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: USA
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Sequence 11, Application US/09086726;
Sequence 11, Application US/09086726;
Patent No. 634673B;
GENERAL INFORMATION:
APPLICANT: Stanley, Christopher John
APPLICANT: Orum, Henrik
APPLICANT: Orum, Henrik
TITLE OF INVENTION: Nucleic Acid Analogs With A Chelating Functionality
FILE REFERENCE: 100382-004086,726
CURRENT APPLICATION NUMBER: US/09/086,726
CURRENT PILING DATE: 2001-07-10
PRIOR FILING DATE: 1996-05-24
PRIOR FILING DATE: 1996-05-24
PRIOR FILING DATE: 1994-11-25
PRIOR FILING DATE: 1993-11-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.0%; Score 12.6; DB 3; Length 36; 78.9%; Pred. No. 2.1e+03; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature
; LOCATION: 1..36
; OTHER INFORMATION: /function= "oligonucleotide 49"
US-08-584-760A-49
APPLICATION NUMBER: 08/211,860
FILING DATE: 15-APR-1994
APPLICATION NUMBER: 08 9121815.6
FILING DATE: 14-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Naomi Biswas
REGISTRATION NUMBER: 38,384
REFERENCE/DOCKET NUMBER: 92H853-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SELECTION:
TELEPRAK: 610/878-4234
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
                                                                                                                                                                          92H853-1
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 78.9
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                              linear
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US-08-584-760A-49/c
US-08-584-760A-49/c
Sequence 49, Application US/08584760A
Fatent No. 6290953
GENERAL INFORMATION:
APPLICANT: Ballance, David J
APPLICANT: Finnis, Christopher J A
APPLICANT: Sleep, Darrell
TITLE OF INVENTION: Medicine
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADRESS:
ADDRESSE: Centeon L.L.C.
STREET: 1020 First Avenue
CITY: King of Prussia
STRET: Dem sylvania
COUNTER: Dem sylvania
COUNTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: RELORD SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT RELABABLE PORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: BM PC compatible
COMPUTER: BM PC Compatible
COMPUTER: BM PC Compatible
COMPUTER: BENDABLE FORM:
MEDIUM TYPE: FLOPPY disk
SOFTWARE: PATENT RELABABLE
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION
FILING DATE:
CLASSIFICATION
CLASSIFICATION
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i LOCATION: 1..35
CHERR INFORMATION: /function= "oligonucleotide 50"
US-08-584-7605-50
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,760A
                                                                                                                                                                            FILING DATE:
CLASSIPTCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/211,860
FILING DATE: 15-APR-1994
APPLICATION NUMBER: GB 9121815.6
FILING DATE: 14-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Naomi Biswas
REGISTRATION NUMBER: 92.H853-1
FLECOMMUNICATION INFORMATION:
TELEPHONE: 610/878/4221
INFORMATION FOR SEQ ID NO: 50: SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: NUCleic acid
STRANDENDESS: Gouble
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Best Local Similarity 78.9°
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: line
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; OTHER INFORMATION: for Codon 508 - wildtype US-09-270-140A-52
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; Sequence 60, Application US/08629001A
; Patent No. 5858661
; GENERAL INFORMATION:
                                                                                                                                                     1 AGTAACATCTATGTTTGGTT 20
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NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 225
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (810) 539-5050
TELEPRAX: (810) 539-5055
INFORMATION FOR SEO ID NO: 60.
SEQUENCE CHARACTERISTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 75.0
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-642-274D-139
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US-08-629-001A-60
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                                                                                                                                                                                                                                                          RESULT 17
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                                                                                                                                                                                                                             ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: 203 Textile Buildling, 119 No. 5587300th Fourth Street
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE: OTHER INFORMATION: Description of Artificial Sequence:wildtype RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fuery, Caroline
APPLICANT: Cairns, Murray
TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
FILE REPERENCE: J6.11799
CURRENT APPLICATION NUMBER: US/09/270,140A
CURRENT RILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 60/079,651
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                GENERAL INFORMATION:
APPLICANT: Malter, James S.
TITLE OF INVENTION: Method to Increase Regulatory Molecule
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muleting, Raasch, Gebhardt & Schwappach, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.0%; Score 12.2; DB 1; Length 34; 82.4%; Pred. No. 3.2e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,130A
FILING DATE: 26-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 119.00010101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 52, Application US/09270140A
Patent No. 6351941
GENERAL INFORMATION:
APPLICANT: Todd, Alison
             RESULT 15
US-08-233-130A-3/c
: Sequence 3, Application US/08233130A
: Patent No. 5587300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGTAACATCTATGTTTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 AGTAATATGTATGTATG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 34 base pairs
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                                                                                                                                                                                                                                                                                                                                   ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                      USA
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US-09-270-140A-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-233-130A-3
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LENGTH: 22
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Sequence 139, Application US/08642274D
Patent No. 6200749
GENERAL INFORMATION:
APPLICANT: Shiloh, Yosef
TITLE OF INVENTION: MUTATED FORMS OF THE ATAXIA-TELANGIECTASIA GENE AND METHOD TO TITLE OF INVENTION: SCREEN FOR A PARTIAL A-T PHENOTYPE
FILE REFERENCE: 229000033
CURRENT APPLICATION NUMBER: US/08/642,274D
CURRENT FILING DATE: 1996-05-03
NUMBER OF SEQ 1D NOS: 220
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                                                      Gaps
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     Length 22;
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                                                                                                                                                                                                                                                                                                                                                                              ATAXIA-TELANGIECTASIA GENE AND ITS
GENOMIC ORGANIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NATH:
APPLICATION NATH:
APPLICATION NUMBER: US/08/629,001A
Query Match 60.0%; Score 12; DB 4; I
Best Local Similarity 35.0%; Pred. No. 3.9e+03;
Matches 7; Conservative 8; Mismatches 5;
                                                                                                                                                                                                                                                                                          ALFULCANT: Shilch, Yosef
TITLE OF INVENTION: ATAXIA-TELANGIECTASIA
TITLE OF INVENTION: GENOMIC ORGANIZATION
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 5858661thwestern Hwy.
CITY: Farmington Hills
STATE: Michigan
COUNTRY: US
                                                   8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Chunakov, I194
TITLE OF INVENDATON: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US 09/22,978
CURRENT FILING DATE: 1999-04-20
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1998-11-23
EARLIER PILING DATE: 1998-11-23
EARLIER PRILIG DATE: 1998-11-23
EARLIER FILING DATE: 1998-04-21
NUMBER: OF SEQ ID NOS: 11796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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US-09-443-199C-847/c
i Sequence 847, Application US/09443199C
j Sequent No. 6670464
j GENERAL INFORMATION:
j APPLICANT: Shimkets, Richard A.
j APPLICANT: Leach, Martin
j TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide
j TITLE OF INVENTION: Polymorphisms and Methods of Use Thereof
j TITLE OF INVENTION: Polymorphisms and Methods of Use Thereof
j CURRENT APPLICATION NUMBER: US/09/443,199C
j CURRENT APPLICATION NUMBER: 60,109,024
j PRIOR FILING DATE: 1998-11-17
j NUMBER OF SEQ ID NOS: 1272
j SOFTWARE: CuraGen Patent Formatter Version 0.9
j SEQ ID NO 847
linenTH: 51
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LOCATION: (26)...(0)

CTHER INFORMATION: 1 of 2 allelic variants (848 is other entry)

NAME/KEY: misc_feature

LOCATION: (0)...(0)

CTHER INFORMATION: Accession number cg43949585

US-09-443-199C-847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.0%; Score 12; DB 4; Length 47; 85.7%; Pred. No. 4.18+03; 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 24
COTHER INFORMATION: 99-15423-223 : polymorphic base G or US-09-422-978-2712
                      US-09-422-978-2712
; Sequence 2712, Application US/09422978
; Patent No. 6537751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGTAACATCTATGTTTGGTT 20
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo Sapiens
                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 2712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Patent No. 5646156
GENERAL INFORMATION:
APPLICANT: Jacobson, Marlene A
APPLICANT: Johnson, Robert G
APPLICANT: Salvatore, Christopher A
TITLE OF INVENTION: INHIBITION OF EOSINOPHIL
TITLE OF INVENTION: ACTIVATION THROUGH A3 ADENOSINE RECEPTOR ANTAGONISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                         CTHER INFORMATION: Description of Artificial Sequence:intronic CTHER INFORMATION: sequence US-08-642-274D-139
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                                                                                                                                                                                                                                   Length 30;
                                                                                                                                                                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Rahway
STATE: New Jersey
COUNTRY: United States
ZIP: 07055
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMpatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,009
FILING DATE: 25-APR-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                 Query Match
60.0%; Score 12; DB 3;
Best Local Similarity 75.0%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 19219
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3901
TELEPAK: (908) 594-4720
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGTAACATCTATGTTTGGTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 139 LENGTH: 30
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Matches 15; Conserv
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US-08-233-009-51
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                                                                                                                        FEATURE:
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IS-09-440-523-61
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Facture No. 6027889

GENERAL INFORMATION:
APPLICANT: Baranty, Francis
APPLICANT: Baranty, Francis
TITLE OF INVENTION: OUTPLED LIGASE DETECTION AND POLYMERASE CHAIN REACTIONS
TITLE OF INVENTION: COUPLED LIGASE DETECTION AND POLYMERASE CHAIN REACTIONS
FILE REPERENCE: 19603/441

CURRENT APPLICATION NUMBER: 06/018,532

CURRENT APPLICATION NUMBER: 60/018,532

EARLIER APPLICATION NUMBER: 60/018,532

MUMBER OF SEQ ID NOS: 76

SOFTWARE PARENTING DATE: 1996-05-29

NUMBER OF SEQ ID NOS: 76

SEQ ID NO 61

EINGTH: 57
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                                                                           GRNERAL INFORMATION:
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Martin
TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide
TITLE OF INVENTION: Polymorphisms and Methods of Use Thereof
TITLE PEPERENCE: 1596-534A
CURRENT APPLICATION NUMBER: US/09/443,199C
CURRENT FILING DATE: 1999-11-16
PRIOR PLING DATE: 1998-11-17
NUMBER OF SEQ ID NOS: 1272
SOFTWARE: CLRAGEN PATENT FORMATTER VERSION 0.9
SEQ ID NO 848
LENGTH: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (26) ... (0)
OTHER INFORMATION: 2 of 2 allelic variants (847 is other entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.0%; Score 12; DB 4; Length 51; 75.0%; Pred. No. 4.2e+03; Live 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature

LOCATION: (0)...(0)

COTATION: (0)...(0)

COTATION: Accession number cg43949585

US-09-443-199C-848
              US-09-443-199C-848/c; Sequence 848, Application US/09443199C; Patent No. 6670464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AGTAACATCTATGTTTGGTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.01
Then 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 60.0
Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 23
US-08-864-473-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-864-473-61
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APPLICANT: Charles Kunsch

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Pannon

TITLE OF INVENTION: Staphylococcus aureus Polymucleotides and Sequences CORRESPONDENCE ADDRESS:

ADDRESSE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: ROCKVILLE

STATE: Maryland
                                                                     APPLICANT: Barany, Francis
APPLICANT: Lubin, Matthew
TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCE DIFFERENCES USING
TITLE OF INVENTION: COUPLED LIGASE DETECTION AND POLYMERASE CHAIN REACTIONS
FILE REFERENCE: 19603/441
CURRENT APPLICATION NUMBER: US/09/440,523
CURRENT FILING DATE: 1999-11-15
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 61
LENGTH: 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Description of Artificial Sequence: Primer ; OTHER INFORMATION: Sequence US-09-440-523-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: AGII TEACT
CURRENT APPLICATION DATA:
FILING DATE: 20-Oct-1997
CLASSIPICATION: UNMORE: 20-Oct-1997
PRIOR APPLICATION: AUMNOWN>
PRIOR APPLICATION: AUMNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.0%; Score 12; DB 3; Length 57; 100.0%; Pred. No. 4.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 60.0%; Score 12; DB Best Local Similarity 100.0%; Pred. No. 4.2 Matches 12; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-956-171E-4982/c; Sequence 4982, Application US/08956171E; Patent No. 6593114; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
Sequence 61, Application US/09440523
Patent No. 6268148
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 TAACATCTATGT 40
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42 AGAAAAGCTATGTATGCTT 61
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                                                                                                                                                                                                                                                                                                 Query Match 60.0%; Score 12; DB 4; Length 58; Best Local Similarity 75.0%; Pred. No. 4.2e+03; Matches 15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                   Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 199, Application US/08303275
Patent No. 5766598
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Tox, William I.
TITLE OF INVENTION: IMMUNOBERICIENCY VIRUS RECOMBINANT
TITLE OF INVENTION: POXVIRUS VACCINE
NUMBER OF SEQUENCES: 205
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,275
                                                                                                                                                                                                     TOPOLOGY: linear
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SEQUENCE DESCRIPTION: SEQ ID NO: 4982:
US-08-956-171E-4982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US 07/897,382
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: FOOMMEY, William S.
REGISTRATION NUMBER: 25,566
REFERRUCE/DOCKET NUMBER: 454310-2420
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
COUNTRY: USA
REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEPAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 4982:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 Dage pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECON. (212) evolution TELEPHONE: (212) evolution TELEPAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 198:
SEQUENCE CHARACTERISTICS:
TRINGTH: 63 bese pairs
                                                                                                                                                                                                                                                                                                                                                                                          1 AGTAACATCTATGTTTGGTT 20
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COmpatible
                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
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Gaps
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Batent NO. 6656731
GENERAL INFORMATION:
APPLICANT: Ribosyme Pharmaceuticals, Inc.
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
FILE REFERENCE: MBH800-884-C
CURRENT FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/444,209
PRIOR PILING DATE: 1999-11-19
PRIOR PLING DATE: 1999-11-19
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-10-22
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                                                                                     APPLICANT: PROJECT, BRZO
APPLICANT: Tartaglia, James
APPLICANT: Tartaglia, James
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS RECOMBINANT
TITLE OF INVENTION: POXVIRUS VACCINE
NUMBER OF SEQUENCES: 205
CORRESPONDENCE ADDRESSS:
ADDRESSEE: C/O William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
CUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.0%; Score 12; DB 1; Length 63; 75.0%; Pred. No. 4.2e+03; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REGISTRANCE/DOCKET NUMBER: 454310-2420
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/897,382
FILING DATE: 11-UN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10036
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
             Sequence 199, Application US/08303275
Patent No. 5766598
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AGTAACATCTATGTTTGGTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELBFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 63 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 63 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 15; Conservative
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US-08-303-275-199/c
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GENERAL INFORMATION:
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Patent No. 5650553
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R. et al.
TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene
TITLE OF INVENTION: and Pathogens
NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5650553ris
STREET: One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 4.8e+03;
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Pred. No. 4.9e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,822A
FILING DATE: 17-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                            4.8e+03;
                                                                                                                                                                                                                               6; Mismatches
PRIOR APPLICATION NUMBER: US 60/059,473
PRIOR FILING DATE: 1997-09-22
NUMBER OF SEQ ID NOS: 1208
SCFTWARE: PatentIn version 3.0
SEQ ID NO 399
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 57, Application PC/TUS9507744A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                          59.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
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86.7%;
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AGUAACUUCUGUGUU 15
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                                                                                                                                                                                     Query Match
Best Local Similarity 46.7
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                              TYPE: RNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Best Local Similarity
Matches 13; Conserv
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US-08-261-822A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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PCT-US95-07744A-57
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Sequence 149, Application US/09287796A

Sequence 149, Application US/09287796A

GENERAL INFORMATION:
APPLICANT: McKay, Robert A.
APPLICANT: Monia, Brett
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Nero, Pam
APPLICANT: Mero, Pam
TITLE OF INVENTION: POR THE MODULATION OF JNK PROTEINS
TITLE OF INVENTION: POR THE MODULATION OF JNK PROTEINS
TITLE OF INVENTION: POR THE MODULATION OF JNK PROTEINS
TITLE OF INVENTION: 1899-04-07
CURRENT APPLICATION NUMBER: 09/130,616
EARLIER APPLICATION NUMBER: 09/130,616
EARLIER FILING DATE: 1998-04-07

EARLIER FILING DATE: 1999-06-07

NUMBER OF SEQ ID NOS: 165
SEQ ID NO 149
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
APPLICANT: Trustees of The University of Pennsylvania
TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene
TITLE OF INVENTION: and Pathogens
UNMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris
STREET: One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 18;
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CUDNIKK: USA

CUNTKK: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07744A
FILING DATE: 15-JUNE-1995
CLASSIFPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,822
FILING DATE: June 17, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y:
REGISTRATION NUMBER: 34,293
TELECOMMUNICATION INFORMATION:
met FOLIAME (716, F.C. 2) 10.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 59.0%; Score 11.8; DB 5;
Best Local Similarity 86.7%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (215) 568-3100
TELERAX: (215) 568-3439
INFORMATION FOR SEO ID NO: 57,
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 CATCTATGTTTGGTT 20
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                         USA
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US-09-287-796-149/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICAN:
APPLICAN: Jan van den Hurk and Peter Tijssen
TITLE OF INVENTION: Bovine Viral Diarrhea Virus Group II
TITLE OF INVENTION: gp53 Compositions and Methods
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,722
   FALLOW AFFILE ALON 1994

FILING DATE: 10-NOV-1994

ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615

REPERENCE/DOCKET NUMBER: 1242-0001.30

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860

TELEPHONE: (415) 324-0860

INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDENDESS: single
TOPOLOGY: linear
MOLECTLE TYPE: DNA
HYPOLOGY: Linear
MOLECTLE TYPE: DNA
HYPOTHETICAL: NO
ANNOT CENTER AND
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STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/445,746
FILING DATE: 22-MAY-1995
APPLICATION NUMBER: US 08/337,618
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-008-722-10
; Sequence 10, Application US/09008722
; Patent No. 6015795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Primer 1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38,615 REPRENCE/DOCKET NUMBER: 124 TELECOMMUNICATION INFORMATION: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 86.7
Matches 13; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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; Sequence 149/C
; Sequence 149, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION;
APPLICANT: McKay, Robert A.
; APPLICANT: Monia, Brett
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
; APPLICANT: Nero, Pam
; APPLICANT: Nero, Pam
; TITLE OF INVENTION: FOR THE MODULATION OF JUK PROTEINS
; TITLE OF INVENTION: FOR THE MODULATION OF JUK PROTEINS
; TITLE OF INVENTION: FOR THE MODULATION OF JUK PROTEINS
; TITLE OF INVENTION: FOR THE MODULATION OF JUK PROTEINS
; TITLE OF INVENTION: FOR THE MODULATION OF JUK PROTEINS
; FILE REPERENCE: 1597+031
; CURRENT APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 149
; LENGTH: 20
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| Sequence 10, Application US/08445746
| Patent No. 5709865
| Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.0%; Score 11.8; DB 3; Length 20; 86.7%; Pred. No. 4.9e+03; tive 0; Mismatches 2; Indels
                                                                                                                                                             Query Match
Best Local Similarity 86.7%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 2; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,746
FILING DATE: 22-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Synthetic sequence
US-09-130-616-149
                                    FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-287-796-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
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Best Local Similarity 86.77
Matches 13; Conservative
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Gaps

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APPLICANT: Skern, Timothy
TITLE OF INVENTION: Expression of Mature Proteinase 2A, the
TITLE OF INVENTION: Partial Purification Thereof and Preparation of Substrates
TITLE OF INVENTION: Having an Inhibitory Effect
NUMBER OF SEQUENCES: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5.556
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,373
FILING DATE: 11-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1225 Connecticut Avenue, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/971,619
FILING DATE: 06-NOV-1992
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2061, Application US/08956171E Patent No. 6593114 GENERAL INFORMATION:
                                                                                                                                            Maurer-Fogy, Ingrid
Sommergruber, Wolfgang
Zophel, Andreas
Blaas, Dieter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                             Sequence 2, Application US/08320373
Patent No. 5559025
GENERAL INFORMATION:
APPLICANT: Ahorn, Horst
                                                                                                                                                                                                                          Kuchler, Ernst
Liebig, Hans-Dieter
Skern, Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Charles Kunsch
Gil H. Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (202) 466-0800
(202) 833-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity 86.7
Matches 13; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                           Ahorn, Horst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, K
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                                           JS-08-320-373-2/c
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APPLICANT:
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TELEX: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sommergruber, Wolfgang
APPLICANT: Sophel, Andreas
APPLICANT: Blass, Dieter
APPLICANT: Blass, Dieter
APPLICANT: Liebig, Hans-Dieter
APPLICANT: Liebig, Hans-Dieter
APPLICANT: Skern, Timothy
TITLE OF INVENTION: Expression of Mature Proteinase 2A, the
TITLE OF INVENTION: Partial Purification Thereof and Preparation of Substrates
TITLE OF INVENTION: Having an Inhibitory Effect
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                                                                                                                                                        Score 11.8; DB 3; Length 29;
Pred. No. 5e+03;
0; Mismatches 2; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,373
FILING DATE: 11-OCT-1994
CLASSIFICATION: 435
PRICK APPLICATION NUMBER: US 07/971,619
FILING DATE: 06-NOV-1992
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 466-0800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1225 Connecticut Avenue, N.W. CITY: Washington COUNTRY. D.C. COUNTRY.
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Sommergruber, Wolfgang
Sophel, Andreas
Blaas, Dieter
Kuchler, Ernst
Liebig, Hans-Dieter
            MOLECULE TYPE: DNA
HYPOTHETICAL: NO
MATI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Primer 1A
US-09-008-722-10
                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1, Application US/08320373; Patent No. 5559025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 466-0800
TELEFAX: (202) 833-8716
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                      59.0%;
                                                                                                                                                                                                                                     GTAACATCTATGTTT 16
                                                                                                                                                                                                                                                                          1 GGAAGATCTATGTTT 15
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                                                                                                                                                                                           13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
-hes 13; Conserv?
linear
                                                                                                                                                      Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20036
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                    RESULT 35
US-08-320-373-1
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CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
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APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-00c1-1997
CLASSIFICATION: <Unknown>
                                                 FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/ACRET INCORMATION:
NAME: MARK J. Hyman
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5031:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4977, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
GII H. Choi
Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                    TELEPHONE: (240) 314-1224
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                                                                                                                                                                                                                                                                                                                                        TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5031:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 DASE pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GTAACATCTATGTTT 16
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PRIOR APPLICATION DATA:
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Matches 13; Conservative
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US-08-956-171E-4977/c
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Steven C. Barabh
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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MEDIUM TYPEL Diskette, 3.50 inch, 1.4MD storage
COMPUTER: HP Vectra 486/33
CORPUTER: HOSTER: CORPUTER: CORPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 11.8; DB 4; Length 50;
Pred. No. 5.2e+03;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 2061:
US-08-956-171E-2061
         STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5031, Application US/08956171E Patent No. 6593114 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (301) 309-843: INFORMATION FOR SEQ ID NO: 2061: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.0%;
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COMPUTER READABLE FORM:
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Best Local Similarity 86.73
Matches 13; Conservative
                                                                         STATE: Maryland
                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-956-171E-5031
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Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
                                                         Gaps
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0
59.0%; Score 11.8; DB 4; Length 54; 86.7%; Pred. No. 5.2e+03; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
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Matches
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Sequence 30, Application US/09462941

Patent No. 6608183

GENERAL INFORMATION:

APPLICANT: Cox III, George N

APPLICANT: Bolder Biotechnology, Inc.

TITLE OF INVENTION: Deliverives of Growth Hormone and Related Proteins

FILE REFERENCE: 4152-1-PUS

CURRENT APPLICATION NUMBER: US/09/462,941

CURRENT PILING DATE: 2000-01-14

PRIOR FILING DATE: 1997-07-14

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 30

LENGTH: 65
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Patent No. 6608183

GENERAL INFORMATION:

APPLICANT: COX.III, George N

APPLICANT: Bolder Biotechnology, Inc.

TITLE OF INVEXTION DELIVATIVES Of Growth Hormone and Related Proteins

FILE REPERENCE: 4152-1-FUS

CURRENT FILING DATE: 2000-01-14

PRIOR PRILING DATE: 1997-07-14

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                   y Match 59.0%; Score 11.8; DB 4; Length 58; Local Similarity 86.7%; Pred. No. 5.2e+03; hes 13; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 11.8; DB 4;
Pred. No. 5.3e+03;
                TYPE: nucleic acid

STRANDEDNESS: double

FOOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 4977:
LENGTH: 58 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.0%;
86.7%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                 2 GTAACATCTATGTTT 16
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Best Local Similarity 86.79
Watches 13; Conservative
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Best Local Similarity
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US-09-462-941-30
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                                                                                                                                     Query Match
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APPLICANT: Simmons, Laura C.
APPLICANT: Simmons, Laura C.
APPLICANT: Yansura, Daniel G.
TITLE OF INVENTION: Methods and Compositions for Secretion of Heterologous Proteir
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laura C.
Daniel G.
Methods and Compositions for Secretion of Heterologous Protein
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 Indels
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5
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IEM PC compatible COMPUTER: EIM PC compatible COMPUTER: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
FILLING DATE:
Mismatches
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23

Landress:

LoseE: Genentech, Inc.

CITY: South San Francisco
SITY: California
CONYER: USA
ZIP: 94080

CONYER:
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: P889
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1489
TELERX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                   Sequence 5, Application US/08398617
Patent No. 5747662
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08398617
Patent No. 5747662
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                     6 CATCTATGTTTGGTT 20
                                                                       43 CATCTATGTTCGTTT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 CATCTATGTTTGGTT 20
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13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Simmons, Lau.
APPLICANT: Yansura, Dan.
TILLE OF INVENTION: Met.)
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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US-08-398-617-6/c
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Sequence 6, Application US/08398615
Patent No. 5840523
GENERAL INFORMATION:
APPLICANT: Simmons, Laura C.
APPLICANT: Yanaura, Daniel G.
TITLE OF INVENTION: Methods and Compositions for Secretion of Heterologous Protein
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSES: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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Pred. No. 5.3e+03;
0; Mismatches 2;
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COMPUTER READBLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IEM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/398,615

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGIESTRATION NUMBER: 35,136
REFRENCE/DOCKET NUMBER: P889
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.0%;
86.7%;
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415/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 67 bases
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Best Local Similarity 86.7.
These 13; Conservative
                               TELEX: 910/371-7169
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 bases
                                                                                                                                                                                                                              13; Conservative
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            415/952-9881
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STRANDEDNESS: single
                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
US-08-398-615-6
                                                                                                                                          linear
TELEPHONE:
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                                                                                                                                          TOPOLOGY:
                TELEFAX:
                                                                                                                                                          US-08-398-615-5
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Sequence 5, Application US/08398615
Sequence 5, Application US/08398615
Fatent No. 5840523
GENERAL INFORMATION:
APPLICANT: Simmons, Laura C.
APPLICANT: Vansura, Daniel G.
TITLE OF INVENTION: Methods and Compositions for Secretion of Heterologous Protein
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 11.8; DB 1;
Pred. No. 5.3e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                    ZIP: 94000
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYGTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: P889
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                     PILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION STATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FILLS, Renee A:
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: P889
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 415/952-9881
TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 67 bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
 California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-398-617-6
                    USA
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                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 44
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셤 ઠ

Search completed: September 23, 2004, 16:44:22 Job time : 59 secs

us-10-798-923a-36.szlm80.rni

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C 5 13.6 68.0 80 28 BH902197 C 6 13.4 67.0 46 28 AZS81263 C 7 13.4 67.0 70 14 CD946310 C 8 13.4 67.0 75 9 AV836725 C 10 13.2 66.0 39 28 BH902806	13.2 66.0 46 28 13.2 66.0 50 29 13.2 66.0 52 14 13.2 66.0 59 28	15 13.2 66.0 79 28 16 13 65.0 76 9 17 12.8 64.0 52 28 18 12.8 64.0 52 28	12.8 64.0 64 9 12.8 64.0 67 28 12.8 64.0 70 29	22 12.8 64.0 73 29 23 12.8 64.0 76 28	12.6 63.0 33 28	12.6 63.0 52 9 12.6 63.0 52 9 12.6 63.0 58 9	29 12.6 63.0 64 12 30 12.6 63.0 66 28 31 12.6 63.0 73 14	12.6 63.0 73 28 12.6 63.0 74 9	12.6 63.0 74 9 12.6 63.0 74 29	12.6 63.0 76 9 12.6 63.0 79 28	12.4 62.0 49 28 12.4 62.0 60 28 12.4 62.0 69 14	12.4 62.0 77 29	44 12.2 61.0 24 29 45 12.2 61.0 40 28	12.2 61.0 43 28 12.2 61.0 46 28	48 12.2 61.0 46 28 49 12.2 61.0 47 9	12.2 61.0 50 9 12.2 61.0 51 28	53 12.2 61.0 53 13 54 12.2 61.0 55 29	12.2 61.0 59 9 12.2 61.0 59 14	57 12.2 61.0 59 14 58 12.2 61.0 62 12	59 12.2 61.0 63 9 61 12.2 61.0 64 9	62 12.2 61.0 64 28 63 12.2 61.0 65 29	12.2 61.0 66 28 12.2 61.0 66 29 12.2 61.0 66 29	67 12.2 61.0 67 14 68 12.2 61.0 69 28	12.2 61.0 69 29 12.2 61.0 70 12 12.2 61.0 70 29	72 12.2 61.0 75 29 73 12.2 61.0 76 10	12.2 61.0 77 28 12.2 61.0 77 29 12.2 61.0 79 10 12 60.0 36 29
GenCore version 5.1.6  Copyright (c) 1993 - 2004 Compugen Ltd.  OM nucleic - nucleic search, using sw model	Run on: September 23, 2004, 15:30:50; Search time 1335 Seconds (Without alignments) 447.373 Million cell updates/sec	Title: US-10-798-923A-36 Perfect score: 20 Sequence: 1 agtaacatctatgtttggtt 20	Scoring table: IDENTITY NUC Gapox 10.0 Gapox 1.0	Searched: 27513289 seqs, 14931090276 residues	Total number of hits satisfying chosen parameters: 375216	Minimum DB seq length: 0 Maximum DB seq length: 80	Post-processing: Minimum Match 0% Maximum Match 100%	Listing first	Latabase: bS1:* 1: em_estba:* 2: em_estbum:*	3: em_estin:* 4: em_estim:* 5: em_estrov:*	6: em_estro.* 7: em_estro.*	8: em_htc:* 9: gb_est1:*	10: gb_est2:* 11: gb_htc:*	12: gb_est3:* 13: gb_est4:*	14: qD est5:* 15: em_estfun:* 16: em_estcom.*				24: em_gss_incs:* 24: em_gss_incs:* 25: em gss_rod:*			icted b e of th	Ã.	Source & Conference & Conferenc	No. Score Match Length DB ID Description	C 1 14.2 71.0 42 29 BX203696 BX203696 Danio rer 2 13.6 68.0 51 29 BX547845 BX547845 Arabidops C 3 13.6 68.0 58 28 BZ287564 BZ287564 SALK 0209 C 4 13.6 68.0 73 28 BH811903 BH811903 SALK_0605

BH902197 SALK 0914
AZ5181263 100369016
CD946310 REL 89 Ge
AV036725 AV036725
AZ995788 ZM0281D15
BH9002806 SALK 1009
AZ646477 IM0512G02
AL937476 Arabidops
CB275049 Kuc2b01.y
BZ384046 SALK 1349
BH613705 SALK 0346
AL682075 AL682075
BH907881 SALK 0446
BH907881 SALK 0446
BH907881 SALK 0641
CA935569 SAUS6D06.
AZ783086 ZM0205063
BH705120 IM0225K08
BH705120 IM0225K03
AZ437102 IM0525K08
BH7052559 IL-BT062-AZ0505
AN05015 ZMLK 0511
BH811539 SALK 1319
AZ66559 IL-BT062-AZ0505
AN050163 ASALK 1319
AZ66559 IL-BT062-AZ0505
AN05018 IM0647009
BH864251 SALK 0531
BH86437 SALK 0539
AL802258 AU055386
CC7526558 NACL--01BG14585 UU09404.X
BH855346 SALK 0859
AZ77410 Arabidops
AZ52655 NACL--01BG14585 UU09404.X
BH855346 SALK 0859
AZ7777 QW94404.X
BH855346 SALK 0859
AZ77707 QW94404.X
BH855346 SALK 0859
AZ826558 ZM0102G05
CC528867 CC1240 387
CC524790 CS729133
CC524790 CS729133
CC524790 CS729133
CC524790 NACL--01BG145539 AAD160ps
CC524790 NACL--01CF32651 AAD160ps
CC544701 AAD160ps
CC544701 OST90141
CC544739 CST90134
CC544701 AAD160ps
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BE530012 GU059131
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/c NN N	SOURCE Danio rerio CRANISM Danio rerio CROCANISM Danio rerio CRANISM Danio rerio CRANISM Danio rerio CRANISM Danio rerio Enkaryota: Merazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; CYDINIOPTERS CAPTINIGAS; Danio.  AUTHORS Humphray.S.J., Huckle,E. and Durham,J.L. AUTHORS Humphray.S.J., Huckle,E. and Durham,J.L. AUTHORS Humphray.S.J., Huckle,E. and Durham,J.L. COURNAL CAPAN.2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Unpublished COWMENT This sequence was generated from the T7 end of BAC 223120. COMMENT This sequence was generated from the T7 end of BAC 223120.  This sequence was generated from the T7 end of BAC 223120.  This sequence ateails: http://www.sanger.ac.uk/Projects/D_rerio/. FRATURES Location/Qualifiers Location/Qualifiers Location/Qualifiers  Location/Qualifier	. <b>.</b>	DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-548H03-020587, genomic survey sequence.  ACCESSION PS47845  ACCESSION BX547845.1 GT:32440665  KEYWORDS  SOURCE  ARADIGOPSIS thaliana (thale cress)  Arabidopsis thaliana (thale cress)  Arabidopsis thaliana (thale cress)  Arabidopsis thaliana (thale cress)  Arabidopsis thaliana (thale cress)  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; spermatophyta; Magnoliophyta; eudicots; spermatophyta; eudicot
AZ663202 1M0542P08 AA907731 0,93912.5 AA427738 1M0209123 CC325169 XL921 Bay AJ235769 AJ235769 BM34282 fW48e01.y BM574161 fx59h05.y BQ077144 fz13b11.y BQ615017 fab21009. AU102956 AU102956 BT005299 fr56f02.y	B1840243 f871d07.7 BQC15523 f827d09. BH065524 SALK 1011 BM025452 f878G02.7 BM025462 f878B02.7 BM025535 f878b05.7 BM025531 f878b05.7 BM02531 f876911.7 BM025311 f876g11.7 BM025311 f876g11.7 BM529195 f47800.7 BM529195 f47508.7 BM530824 f71508.7 BM530824 f717008.7 BM530824 f87601.7 BM7021179 n271g07.8 B1702944 f866d08.7 B1702944 f866d08.7 B1702944 f866d08.7 B1702912 f866f08.7 B1702912 f866f08.7 B1705319 f857812.7 B1705319 f857805.7 B1705319 f857805.7 B1705319 f857805.7	B183414 E867910.Y B1840013 fs68C01.Y B1840101 fs70d04.Y B1840206 fs70h01.Y BM025294 fs76f02.Y BM025435 fs78e05.Y BM025507 fs79f07.Y BM025703 fs82b03.Y BM185197 fw43a11.Y BM18197 fw31f01.Y BM186911 fv79e09.Y BM187146 fv82f08.Y	
8 6 8 8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	50 12 B1840243 50 13 B0615523 50 28 BH866524 51 12 BM025460 51 12 BM025460 51 12 BM025463 51 12 BM025463 52 12 BM025416 52 12 BM72311 52 12 BM72311 52 12 BM52319 52 12 BM52319 53 12 BM52313 53 12 BM52313 53 12 BM52313 53 12 BM52313 53 12 BM72867 53 12 BM72867 53 12 BM72867 53 12 BM72867 53 12 BM72868 53 12 BM702768 53 12 BM702768 53 12 BM70291 53 12 BM70291 53 12 BM705112 53 12 BM705112 53 12 BM705112 53 12 BM705112 53 12 BM705112 53 12 BM705112		
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Arabidopsis thaliana
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                         16;
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BH811903/c
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                Submitted (01-JUL-2003) Weisshaar B., Max-Planck-Institut fuer Submitted (01-JUL-2003) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At590430. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:

http://www.mpiz-koeln.mgg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                      /clone="GKS-548H03-020587"
/clone="GKS-548H03-020587"
/clone="GKS-548H03-020587"
/note="FGK was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pACI61. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence processed for submission. T-DNA derived sequences were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BZ287564 58 24-OCT-2002 SALK 020942.48.40.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_020942.48.40.x, genomic
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
1 (bases I to 58)
1 (bases I to 58)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Bcker, J.R.,
A Sequence-Indexed Library of Insertion Mutations in the
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                         /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:3702"
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80.0%;
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Class: TDNA tagged.
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BZ287564/c
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organism="Arabidopsis thaliana"

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BH811903 73 bp DNA linear GSS 02-MAY-2002 SALK 060502 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_060502, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shim,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db xref="taxon:3702"
/clone="SAIK 060502"
/clone=lib="Ārabidopsis thaliana TDNA insertion lines"
/clone lib="Ārabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Joseph R. Bcker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute Genomic Analysis Laboratory
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
FERS 858 538 799
Email: ecker@salk.edu
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                                                                                                                                                                                                                                                                                                                                                                                                               68.0%; Score 13.6; DB 28; ilarity 80.0%; Pred. No. 4.6e+04; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.0%; Score 13.6; DB 28; 80.0%; Pred. No. 4.7e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .73
/organism="Arabidopsis thaliana"
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/strain="Columbia 0"
/strain="Columbia 0"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 ATTATTTCTATGTTTGGTT 16
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Best Local Similarity 80.0
Matches 16; Conservative
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10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF1290721.), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 15-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 70)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWP42Inv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                     Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb
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REL 89 GeneTagl Zea mays cDNA, mRNA sequence.
CD946310
                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0369 row: N column: 16
Seq primer: CACACAGGAACAGGTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
                                                                                                                              plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 46.
Location/Qualifiers
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Best Local S
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          AUTHORS
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                                                                                                                   SALK 091447 41.05.x Arabidopsis thaliana TDNA linear GSS 04-SEP-2002 Arabidopsis thaliana genomic clone SALK 091447.41.05.x, genomic BH902197
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1M0369N16R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/clone="SALK 091447.41.05.x"
/clone="SALK 091447.41.05.x"
/clone lib="Ārabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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This is single pass sequence recovered from the left border of
TDNs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/strain="Columbia 0"
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Location/Qualifiers
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       ||| ||||||||||| | || agreacatctatetaagatt 31
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AZ581263.1 GI:11696100
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80.0%;
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Tel: 801 585 5606
Fax: 801 585 7177
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AZ995788
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KEYWORDS
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AV836725 K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare seedling leaves second leaf stage Hordeum vulgare subsp. vulgare_cDNA clone basdla13, mRNA sequence.
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 75)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="seedling leaves"
/dev_stage="second leaf stage"
/clone_lib="K. Sato unpublished cDNA library: Hordeum
vulgare subsp. vulgare seedling leaves second leaf stage"
                    Genoplante, a major partnership french program in plant genomics Unpublished (2003)
                                                                                                                                                     This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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Contact: Kazuhiro Sato
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Bmail: kazsato@rib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp/barley/
database:http://www.rib.okayama-u.ac.jp/barley/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                               67.0%; Score 13.4; DB 14; Length 70; 93.3%; Pred. No. 5.8e+04; ive 0; Mismatches 1; Indels C
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                                                                                             93, rue Henri Rochefort 91025 BVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 13.4; DB 9;
Pred. No. 5.8e+04;
0; Mismatches 2;
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cultivar="Haruna Nijo"
/cultivar="Haruna Nijo"
/sub_species="tulgare"
/db_xref="taxon:112509"
/clone="basdla13"
                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4577"
/clone_lib="GeneTag1"
                                                                                                                                                                                                                                                          /organism="Zea mays"
                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/cultivar="mixture"
                                                                                                                                                                                                                       Socation/Qualifiers
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Best Local Similarity 87.5%;
Matches 14; Conservative
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                                                       Contact: Genoplante
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  Genoplante.
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AV836725/c
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ORGANISM
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AUTHORS
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JOURNAL
AUTHORS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwapt (gil-#1732114 [gb] ART25072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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   GSS 27-APR-2001
                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 31)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb Unpublished (2000)
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/lab host="E. coli strain XLIO-Gold, Tl-resistant, F-"
/lab host="E. coli strain XLIO-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
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AZ995788 31 bp DNA linear GSS 27-APR-200
2M0281D15R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0281D15 R, genomic survey sequence.
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83.3%; Pred. No. 6.4e+04;
trive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Std Error: 0.00
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Seq primer: CACACAGGAAACAGCTATGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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Location/Qualifiers
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/clone="UUGC2M0281D15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                             AZ995788.1 GI:13867015
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Best Local Similarity 83.33
Matches 15; Conservative
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligomuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAP(2 [qi] 4712114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Washidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                               Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse, whole genome scaffolding with paired end reads from 10kb
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Pred. No. 6.7e+04;
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Plate: 612 row. G column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
                                                                                                                                        plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 46.
Location/Qualifiers
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/clone="UUGC1M0512G02"
                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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83.3%;
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Best Local Similarity
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84112, USA
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                AUTHORS
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Alonso, J. M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome

L Unpublished (2001)

Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752
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                                                                                                                                                                        BH902806 39 bp DNA linear GSS 04-SEP-2002 SALK 100993.19.05.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_100993.19.05.x, genomic
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 46)
                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
Mukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db xref="taxon:3702"
/clone="SALK 100993.19.05.x"
/clone="SALK abdidopsis thaliana TDNA insertion lines"
/clone lib="Ārabidopsis thaliana lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At5gl2870.
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/mol type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (thale cress)
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/strain="Columbia 0"
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                     AGTGACATGTGTGTTTGG 18
                                                                                                                                                                                                                                                                                                                BH902806.1 GI:22713922
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15; Conservative
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                                                                                                                                                                                                                                                               survey sequence.
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Best Local Similarity
Matches 15; Conserv
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AZ646477/c
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Enail: est@watson.wustl.edu
The library was constructed by Claire Murphy and Dr. James McCarten
at Washington University, St. Louis. This is a Oligo(dT)-SLI PCR
based library. CDNA PCR products of size >400 nucleotides
containing SLI on the 5' end and oligo(dT) on the 3' end were
nor-directionally cloned into pCRII-TOPO(Invitrogen) following the
TOPO TA cloning protocol. Parasitic adult females were collected
from immunologically naive animals and provided by Dr. Mark Viney
(Mark Viney@bristol.ac.uk) of University of Bristol, Bristol, UK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCRII-TOPO (Invitrogen); Site_1: BCORI;
Site_2: BCORI, The library was constructed by Claire
Murphy and Dr. James McCarter at Washington University,
St. Louis. This is a Oligo(dT)-SLI PCR based library. CDNA
PCR products of size 440 nucleotides containing SLI on
the 5' end and oligo(dT) on the 3' end were
non-directionally cloned into pCRII-TOPO(Invitrogen)
following the Topo TA cloning protocol. Parasitic adult
females were collected from immunologically naive animals
and provided by Dr. Mark Viney (Mark.Viney@bristol.ac.uk)
of University of Bristol, Bristol, UK."
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Strongyloides ratti PA female naive SL1 TOPO
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   Unpublished (1999)
Contact: McCarter Up
The Mashington Univ. Nematode EST Project, 1999
Washington University School of Medicine
Washington Barkway, Box 8501, St. Louis, MO 63108, 7el: 314 286 1800
Fax: 314 286 1810
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Best Local Similarity 83.3%; Pred. No. 6.9e+04;
Matches 15; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Strongyloides ratti"
/mol_type="mRNA"
/db_xref="taxon:34506"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="Parasitic adult"
/lab_host="DH10B"
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The vector to vector length is 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: SL1 primer.
Location/Qualifiers
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Unpublished (2001)
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Strongyloides ratti
Strongyloides ratti
Strongyloides ratti
Eukaryota; Menatoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloidides; Strongyloides.

I (bases 1 to 52)
McCarter, J., Cliffon, S., Chiapelli, B., Pape, D., Martin, J.,
Wylie, T., Dante, M., Marra, M., Hillier, L., Knoaba, T., Theising, B.,
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
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/clone="igh="taxon:1302"
/clone="igh="taxon:1302"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (21-00T-2002) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone F14013. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on the availability can be found at:
                                                                                                                                                                                                                                                                                                 Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
                                       Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
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                                                                      and Weisshaar, B.
A pipeline for automated high-throughput generation of F(flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
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/strain="Columbia 0"
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AL682075
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/organism="Arabidopsis thaliana"
/organism="Arabidopsis thaliana"
/strain="Columbia Go"
/db_xref="taxon:3702"
/db_xref="Taxon:3702"
/clone="SALK 134985.22.65.x"
/clone="SALK 134985.22.65.x"
/clone="SALK was performed on Arabidopsis thaliana lines"
/note="PCR was performed on Arabidopsis thaliana lines acch of which contains one or more TUNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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BH613705
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bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., dadrinab,C., Jeeke,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R. A Sequence-Indexed Library of Insertion Mutations in the
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 533 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
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/mol_type="genomic DNA"
/strain="Columbia 0"
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/clone="SALK_034815"
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83.3%;
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Unpublished (2001)
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Class: TDNA tagged
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                                                                                                                                                                             Class: TDNA tagged
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BH613705/c
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AL682075 AGC-gastrula Silurana tropicalis cDNA clone TGas058j17 5',
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Email: trop@sanger.ac.uk
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
constructed by Aaron M. Zorn.
constructed by Aaron M. Zorn.
constructed by Aaron M. Sorn.
EcoRI.NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site 1: EcoRI; Site 2: NotI
Host: Escherichia coli XL1-blue
                 elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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| lab_host="Escherichia coli XL1-blue" |
| clone lib="XGC-gastrula" |
| force="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 76)
Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
On Mar 18, 2002 this sequence version replaced gi:19538449.
Contact: Taylor R
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each of which contains one or more TDNA insertion
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TROPICALIS_SEQUENCE ID: TGas058j17.plcSP6
Sequencing primer: SP6.
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/mol_type="mRNA"
/db_xref="taxon:8364"
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100.0%; Pred. No. o...
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                                                                                                                                                                                                                                                                                                                                            29 TAACCICTITGILI | |
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USA

LOCUS

TITLE

COMMENT

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Contact: Sobern Exp. (1999)

Contact: Shear R. (1999)

Shoemaker, R. (1999)

Shoemaker, R. (1999)

Shoemaker, R. (1999)

Shoemaker, R. (1999)

Shours, Y. (1999)

Shours, Y. (1999)

Shours, Y. (1999)

Shours, R. (1999)
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64 bp mRNA linear EST 30-NOV-2001
sb38ell.yl Gm-c1013 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1013-357 5' similar to SW:G3PC DIAGA P34913 GLYCERALDEHYDE
3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                           This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At5g54840. Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand This clone is
available through: ResGen, Invitrogen Corp. 2130 South Memorial
Parkway Huntsville, AL 35801 For further information call:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clome="SALK_059062"
/clome lib="Ārabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TET: 314 286 1800
Fax: 314 286 1810
  A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome Unpublished (2001)
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                                                                                        Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIG:
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037,
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
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87.5%; Pred. No. 1e+05;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Arabidopsis thaliana"
|mol_type="genomic DNA"
|strain="Columbia 0"
|db_xref="taxon:3702"
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Matches 14; Conservative
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                                                     BH907881 SALK 044616.22.70.x Arabidopsis thaliana TDNA insertion lines Arabidopsis clone SALK_044616.22.70.x, genomic
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spernatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                       Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
dadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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1 (bases I to 52)
Alonso,J.W., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
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/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 888 558 640 x1752
Fax: 888 558 640 k10 x1752
Fax: 888 558 638 4100 x1752
Fax: 888 558 638 4100 x1752
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/strain="Columbia 0"
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Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission

L Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CBiO 18A, B-mail: barrell@sanger.ac.uk and
hl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, M. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRED927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (+ kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects.
Barrell, Oxford University Press, 1999).
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Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                       /sex="Male"
/lab host="E, Coli strain XL10-Gold, T1-resistant, F-"
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T. brucei sheared genomic DNA clone 26h12, forward sequence,
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Bukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae,
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                      'organism="Mus musculus"
                                                           'mol_type="genomic DNA"
'strain="C57BL/6J"
                                                                                                                      /db_xref="taxon:10090"
/clone="UUGC2M0024C04"
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                                                                                                                                                                                                              /mol type="mrRNA"
// db xref="mrRNA"
// db xref="mrRNA"
// clone="Growner sysTrems" (LONE ID: Gm-cl013-357"
// clone="Growner sysTrems" (LONE ID: Gm-cl013-357"
// tissue type="Whole seedlings, 2-3 week old seedlings,
greenhouse grown"
// lab host="kll0-Gold"
// lone lib="Gm-cl013"
// clone lib="Gm-cl013"
// clone lib="Gm-cl013"
// clone lib="Gm-cl013"
// clone lib="Gm-cl013"
// rhis cDNA library was constructed from mRNA isolated from whole seedlings of 2-3 week old greenhouse grown plants. The cDNA library was prepared using the Stratagene plants. The cDNA library was prepared using the Stratagene plants. The cDNA library was prepared using the Stratagene plantescript IX R cDNA library construction kit.
Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a xhoI restriction site of the pBluescript vector. The blunt-ended cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XLIO-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Brpelding."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Daess 1 to 67)

Si (Daess 1 to 67)

Dunn, Da., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. inngey, A., von Niederhausern, A. and Wright, D., Weiss, R. inngey, A., von Niederhausern, A. and Wright, D., Weiss, R. inngey, A., von Contact: Robert B. Weiss

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT B4112, USA.
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2M0024C04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0024C04 R, genomic survey sequence.
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(800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1417 Std Error: 0.00
Seq primer: -40RP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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Insert Lengdh: 10000 Std Error: 0.00
Plate: 0024 row: C column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 67.
Location/Qualifiers
                                                                                                                                                                                              'organism="Glycine max"
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Fax: 801 585 7177
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GSS 24-FEB-2003
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
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1M0225K08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0225K08 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bobydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 76)
Oh,S.W., Kingsley,T., Shin,H., Zheng,Z., Chen.H.W., Chen,X.,
Wang,H., Ruan,P., Moody,M. and Hou,S.X.
A P-element-insertion screen identified mutations in 450 novel
                                                            Gaps
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/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon: 7227"
/clone="1(2)SH1233"
/clone_lib="P-element-insertion screen"
     Query Match 64.0%; Score 12.8; DB 29; Best Local Similarity 87.5%; Pred. No. 1.1e+05; Matches 14; Conservative 0; Mismatches 2;
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ilarity 87.5%; Pred. No. 1.1e+05;
Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1050 Boyles St., Frederick, MD 21702, USA Tel: 1-301-846-7314
Fax: 1-301-846-6145
                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes in Drosophila
Genetics 163 (1), 195-201 (2003)
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Location/Qualifiers
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Mus musculus
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                                                                                                         5 ACATCTATGTTTGGTT 20
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Lab. of Immunobiology
NCI-FCRDC
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Strizbov, N., Li, Y., Rosso, M. and Weisshaar, B.
Direct Submission

Direct Submission

Submitted (07-MAR-2003) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence is recovered from the left border of the T-DNA. It
indicates an insertion within the locus defined by clone FSEIJ9. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German

Plant Genomics program designated 'GABI'. Information on line

availability can be found at:

http://www.mpiz-koeln.mgg.de/GABI-Kat/,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana T-DNA flanking sequence GK-389F02-018268,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
| note="PCR was performed on DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pAC16. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence were processed for submission. T-DNA derived sequences were
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H. and Weisshaar, B.
                                                                                                                                                                                                                                                             Gaps
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0
                                                                                                                                                                                                64.0%; Score 12.8; DB 29; Length 70; 87.5%; Pred. No. 1.1e+05; ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
1. .70
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
strain="TREU927"
/db_xref="taxon:5691"
/clone="26h12"
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/clone="GK-389F02-018268"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (thale cress)
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                                                                                                                                                                                                                                                                                                                                                    44 AACATCTATGTGTTGT 29
                                                                                                                                                                                                                                                     14; Conservative
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                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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                                                                                                                                                                                                     Query Match
     source
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 22
BX286255/c
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AUTHORS TITLE

JOURNAL REFERENCE JOURNAL REFERENCE

AUTHORS JOURNAL

TITLE

COMMENT

FEATURES

ORIGIN

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Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA935569 51 bp mRNA linear EST 30-DEC-2002 sau56b06.yl Gm-c1071 Glycine max cDNA clone SOYBEAN CLONE ID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shoemaker, Reim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="SALK 04174.25.60.x"
/clone="SALK 04174.25.60.x"
/clone="Ib="Arabidopsis thaliana TDNA insertion lines"
/clone="Ick was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 3' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
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                                                                                                                                         Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Pax: 858 558 558 6379
Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.0%; Score 12.6; DB 28;
78.9%; Pred. No. 1.2e+05;
ive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic_DNA"
/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gm-c1071-4692 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA935569
CA935569.1 GI:27424049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine max (soybean)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: TDNA tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 78.9
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycine max
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AUTHORS
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JOURNAL
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CA935569
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KEYWORDS
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                                                                    TITLE
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                                                                                                                                                        COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis vector DNA was prepared from a derivative of pwn42 gql 4732114[94]APIAPIOT2.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BH792403 33 bp DNA linear GSS 02-APR-2002 SALK 064174.25.60.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_064174.25.60.x, genomic
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1 (Dases 1 to 33)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD4Zny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                   S. 2030 E., SLC,
        Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                Rm. 308, Biomedical Polymers Research Bldg., 20
84112, USA
                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0225 row: K column: 08
Seq primer: CGTrGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 77.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
                                                                                               Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db xref="taxon:10090"
clone="UUGC1M0225K08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       survey sequence.
BH792403
BH792403.1 GI:19889138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 TAACATCTATGTTTGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sex="Male"
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Best Local Similarity 8/...
Best 14; Conservative
                                                                       plasmid inserts
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plate of this clone contains both human and mouse derived clones. Thus, the origin of this clone is uncertain. This caution should be kept in mind should you use this clone.
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/dev_stage="two to six-week old"
/clone_lib="Arabidopsis thaliana aboveground organs two to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 58)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                               AV518688 Arabidopsis thaliana aboveground organs two to six-week old Arabidopsis thaliana clone APD36a04F 3', mRNA sequence.
                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Possible reversed clone: similarity on wrong strand Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Jun 23, 2000 this sequence version replaced gi:8678215.
Contact: Brika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.0%; Score 12.6; DB 9; 78.9%; Pred. No. 1.3e+05; tive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                              1. .52
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                            /db_xref="GDB:3916845"
                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:525416"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:3702"
/clone="APD36a04F"
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/strain="Columbia"
                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Matches 15; Conserv
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AV518688/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
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TITLE
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PUBMED
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                                                                                                                                                                                                                                                                                                                              Jab host="DH10B"
/clone lib="Gm-c1071"
/note="Wector: pSPORT1; Site 1: NotI; Site 2: SalI; The
cDNA library was constructed from mRNA isolated from
immature pods (approximately 2cm long) of greenhouse grown
plants. The library was prepared using the Life
Technologies pSuperScript cDNA library construction kit.
Complementary DNA was synthesized from mRNA using a
poly(dT) sequence with a NotI restrictions site. SalI
linkers adapters were ligated to the blunt-ended cDNA
fragments followed by NotI digestion. The cDNA fragments
were directionally cloned into the NotI-salI restriction
site of the pSPORTI vector. The ligated cDNA fragments
were transformed into E.coli ElectroMax DH10B host cells.
This library was constructed in the laboratory of Dr. Lila
VodXin by Anu Khanna at the University of Illinios at
Urbana-Champaign. email: l-vodkin@uluc.edu"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 52)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Ghissoe,S., Dietrich,M., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,M.,
Mardis,R., Moore,B., Worris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA065015

zml2c05.rl Stratagene pancreas (#937208) Homo sapiens cDNA clone
IMAGE:525416 5' similar to TR:G545018 G545018 BRG1=BRAHMA HOMOLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                           /clone="SOYBEAN CLONE ID: Gm-c1071-4692"
/tissue_type="immature pods (~2cm long) of greenhouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
call: (800)-533-4363 or contact: ccu@resgen.com web site:
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.0%; Score 12.6; DB 14; Length 51; 78.9%; Pred. No. 1.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID:
                                                                                                                                                                                organism="Glycine max"
                                                Putative full length read
vector to vector length is 52
Seq primer: -40RP from Gibco.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                              grown plants"
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AA065015.1 GI:1558631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Conservative
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314 286 1810
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Length 52; Indels EST 29-SEP-2000

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1 AGTAACATCTATGTTTGGT 19
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                                                                                                                                                                                                                      BI097343
SWOV3MCAM61F08SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM61F08 5',
          /note="Vector: pBluescript11 SK-; Site_1: EcoRI; Site_2:
XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecular Parasitology
Smith College Department of Biological Sciences
Smith College Department of Biological Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135833826
Fax: 4135833826
Example General Sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="molting L3"
/lab.host="XL1-Blue MRF'"
/clone lib="Onchocerca volvulus molting L3 larva cDNA
(SL96MEW-OvmL3)"
                                                                                                                                                                                                                                                                                                                                                                           (Dases 1 to 64)
Williams,S.A., Lizotte-Waniewski,M., Laney,S. and Lustigman,S. Genes expressed in molting L3 larvae of Onchocerca volvulus Unpublished (1997)
Contact: Steven A. Williams
                                                                                                Gaps
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0
                                                                 Score 12.6; DB 9; Length 58;
Pred. No. 1.3e+05;
                                                                                              Indels
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/organism="Onchocerca volvulus"
/mol type="mann"
/strain="Kumba, Cameroons"
/db.xref="reaxon:6282"
/clone="SWOv3MCAM61F08"
                                                                                                4;
                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                  Onchocercidae; Onchocerca.
                                                                                                                          2 GTAACATCTATGTTTGGTT 20
                                                                                                                                                 40 GTAACTTGTATGATTGATT 22
                                                                                                                                                                                                                                                                                           BI097343.1 GI:14549000
six-week old"
                                                                    63.0%;
78.9%;
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                                                                                                                                                                                                                                                                                                                                      Onchocerca volvulus
                                                                                                15; Conservative
                                                                                                                                                                                                                                                                  mRNA sequence.
BI097343
                                                                   Query Match
Best Local Similarity
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Gaps

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63.0%; Score 12.6; DB 12; Length 64; 78.9%; Pred. No. 1.3e+05; ive 0; Mismatches 4; Indels (

15; Conservative

Query Match Best Local Similarity Matches 15; Conserv

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis vector DNA was prepared from a derivative of pWNA2 (gil 47321141gbl AR129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT 84112, USA
   GSS 13-DEC-2000
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 66)
AZ630914 66 bp DNA linear GSS 13-DEC-200
1M0485A05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                 Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                        clone UUGC1M0485A05 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bmail: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plate: 0485 row: A column: 05
Seg primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db xref="taxon:10090"
/clone="UUGCIM0485A05"
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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A1904585 130-MAR-2000 14 bp mRNA linear EST 30-MAR-2000 IL-BT062-191298-010_1 BT062 Homo sapiens CDNA, mRNA sequence.
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Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/seq/gethtml.pl?tl=IL&t2=IL-BT062-010_1.ht
Bmail: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Peverse complemented post-ligation sequence from source sequence.
Class: transposon-tagged.
Location/Qualifiers
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 73;
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AGTAACTGTTCTGTTTGGT 54
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Homo sapiens
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Matches 15; Conserv
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1 (bases 1 to 73)
Walbot, V.
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                                                                                                                                                                                                                                                                                                                                                                                                                          93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
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855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
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Pred. No. 1.4e+05;
0; Mismatches 4;
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/clone="BN25063E12"
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/cultivar="Jet neuf"
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                                 43 AGTAGCTTCTGGGTTTGGT 61
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1 AGTAACATCTATGTTTGGT
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1 Similarity 78.9%;
15; Conservative (
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Genoplante
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Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
                                                                                                                                                                                                                                                                                                                  15; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 74)
Dias B. To 74)
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
Go'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
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Email: asimpson@ludwig.org.br

Email: asimpson@ludwig.org.br

Project. This ener derived from the FAPESP/LICR Human Cancer Genome

Project. This enery can be seen in the following URL

(http://www.ludwig.org.br/seq/gethtml.pl?tl=IL&t2=IL-BT062-011.html

&t3=311298&t4=1)

Seq primer: puc 18 forward.

Location/Qualifiers
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/clone_lib="BT062"
/note="Organ: breast; Vector: puc18; Site_1: Smal; Site_2:
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
ml&t3=191298&t4=1)
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DR17E12S 74 bp DNA linear GSS 27-NOV-2002
Danio rerio genomic clone DKEY-17E12, genomic survey sequence.
AL734254
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Arabidopsis thaliana T-DNA flanking sequence GK-759A06-023802,
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Smal; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
I (bases 1 to 74)
Humphray, S. J., Huckle, E. and Hunt, S. E.
Direct Submission
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Further details: http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
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/tissue_type="Testis"
/note="vector pIndigoBAC-536"
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/db_xref="taxon:7955"
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/organism="Danio rerio"
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BX896687
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cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 79)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thallana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnollophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="tumor, 5 pooled (see description)"
/lab_host="nbnl0B"
/clone lib="NCI CGAP_Ov35"
/ibc="Organ: ovary; Vector: pCWV-SPORT6; Site_1: Sall;
Site_2: Not1; This library represents the normalized
version of NCI CGAP_Ov23. Cloned unidirectionally.
Primer: Oligo dT. Average insert size 0.86 kb. Tumor
types include: mixed Mullerian tumor, papillary serous,
clear cell, spindle cell. All are primary tumors,
metastasis positive. Constructed by Life Technologies."
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Arabīdopsis thaliana genomic clone SALK_131965.28.05.n, genomic
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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/wol_type="genomic DNA"
                                                                                                                                                                                      www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                Trace considered overall poor quality Insert Length: 254 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2292458"
                                                                                                                                                                                                                                                                                        Insert Length: 254 Std Error:
Seg primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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78.9%;
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BZ358128
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (15-DEC-2003) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone t3f17. The sequences are generated at the MP1 for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:

| Location/Qualifiers | Location/Qualif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone='GK-759A66'023802"
/clone='GK-759A66'023802"
/clone lib="Arabidopsis thaliana T-DNA insertion lines"
/clone lib="Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pACife! The lines contain one or more T-DNA insertions. The DNA fragment(8) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence were processed for submission. T-DNA derived sequences were
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                                                                                                                                                                                             Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics Unpublished
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1 (bases 1 to 76)
NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
and Weisshaar,B.
A pipeline for automated high-throughput generation of FSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
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                                                                                                                                                                                                                                                                                                                                                      3 (bases 1 to 75)
Rosso, M., Li, Y., Strizhov, N. and Weisshaar, B.
Direct Submission
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/strain="Columbia 0"
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78.9%;
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Unpublished (1997)
                                                                                                  transformed lines
Unpublished
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Best Local Similarity 78.9
Matches 15; Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Eukaryota; Viridiplantae; Streptophyta; Core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Tosids; Eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 60)

2 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinah, C., Jaske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)

Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 558 6379
Email: ecker@salk.edu
adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agazose gal electrophoresis. Vector DNA was prepared from a derivative of pWD12 (gi[4732114]gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheard, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli into (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1251 60 bp DNA linear GSS 05-AUG-2002 095643 Arabidopsis thallana TDNA insertion lines Arabidopsis
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                                                                                                                                                                                                                                                                                                                                Length 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Arabidopsis thaliana"
/wol_type="genomic DNA"
/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (thale cress)
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Best Local Similarity 92.9%;
Matches 13; Conservative
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     /strain="Columbia 0"
/db xref="taxon:3702"
/clone="SALK 11365.28.05.n"
/clone=lb="Ārabidopsis thaliana TDNA insertion lines"
/clone_lb="Ārabidopsis thaliana TDNA insertion lines ach of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Dunn, D., Aoyai, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ665591
1M0547D09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0547D09 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from the Jackson
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                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Insert Length: 10000 Std Brror: 0.00
Plate: 0547 row: D column: 09
Seq primer: GGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 49.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches

    .49
    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

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/clone="UUGC1M0547D09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
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78.9%;
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                                                                                                                                                                                                                                                                                                                                                                                     15; Conservative
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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84112, USA
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CB911682 79 bp mRNA linear EST 25-APR-2003 VVD134E08 373255 An expressed sequence tag database for abiotic stressed berries of Vitis vinifera var. Chardonnay Vitis vinifera CBNA clone VVD134E08 5, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="berries"
/dev_stage="mixed; 8, 9, 11, 13, 15, 16 weeks daf"
/dev_stage="mixed; 8, 9, 11, 13, 15, 16 weeks daf"
/clone lib="An expressed sequence tag database for abiotic
stressed berries of Vitis vinifera var. Chardonnay"
/note="Weotor: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
                                                                                          Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9,392(6676):608-11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 79)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    database for abiotic stressed berries of
                          Lexicon Genetics Incorporated 4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: materials@lexgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                    62.0%; Score 12.4; DB 29; Length 77; 86.7%; Pred. No. 1.7e+05;
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                                                                                                                                                                                                                                                                                                                           /cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                     1. .77 /organism="Mus musculus"
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PCR PRimers
FORWARD: T3 20mer
BACKWARD: T7 21mer (backward)
Plate: 134 row: E column: 08
Seq primer: T3 20mer
High quality sequence stop: 79.
Location/Qualifiers
e
                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="129SV/EV"
/db_xref="taxon:10090"
/clone="0ST275491"
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An expressed sequence tag databar
Vitis vinifera var. Chardonnay
Unpublished (2002)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
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/db_xref="taxon:29760"
/clone="VVD134E08"
                                                                                                                                                                  Location/Qualifiers
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Tel: 775-784-1918
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                                                                                                                                     Class: Gene Trap.
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Mus musculus

Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 77)

Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,

Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A., Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Spaxks,M.J., Van Sligtenhorst,II., Vogel,P., Walke,W., Xu,N.,

Zhu,Q., Person,C. and Sands,A.T.

Whkl kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Contact: Zambrowicz BP

Contact: Zambrowicz BP
                                                                                                              CD903663 69 bp mRNA linear EST 14-JUL-2003 G356.110P16F010919 G356 Triticum aestivum cDNA clone G356110P16, CD903663
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                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae, Triticeae, Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                             Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence has been generated in the framework of the franch plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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OST275491 Mus musculus 129SV/Ev Mus musculus genomic clone
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/tissue_type="grain (356 degrees per day after
pollination)"
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Pred. No. 1.7e+05;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Triticum aestivum"
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                                                                                                                                                                                                                                                    Triticum aestivum (bread wheat)
Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/cultivar="recital"
/db_xref="taxon:4565"
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                                                                                                                                                                                                      CD903663.1 GI:32677991
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Best Local Similarity 92.9%;
Matches 13; Conservative (
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37 ATCTATGTTTGGCT
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2M0003A19F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0003A19 F, genomic survey sequence.
                                                                                                                                                                                                                                      TAGA05P 24 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 6a05, forward sequence, genomic
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Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTAT 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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  Score 12.4; DB 14; Length 79;
Pred. No. 1.7e+05;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .24
/organism="Trypanosoma k
/mol_type="genomic DNA"
/strain="TREU927"
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/clone="6a05"
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AZ774210.1 GI:12899399
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      62.0%;
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(bases 1 to 24)
                                                13; Conservative
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Query Match
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Matches 13; Conserv
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pMPA2 (grl 47321141gbl A7129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reil, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R., Tingey, A., von Diamid laserts and Wright, D. Weiss, R., Dupublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Genome Center University of Utah Holymers Research Bldg., 20 S. 2030 E., SLC, UT 8412, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PW042nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jacksor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.00
                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Pax: 801 585 7177
Pax: 801 585 7177
Pax: 801 585 7177
Pax: 801 503 704
Pate: 0.003 row: A column: 19
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Std Error:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="genomic DNA"
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/clone="UUGC2M0003A19"
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Location/Qualifiers
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model	September 23, 2004, 13:59:29; Search time 1263 Seconds (without alignments) 686.350 Million cell updates/sec	US-10-798-923A-36		IDENTITY NUC Gapop 10.0 , Gapext 1.0	3470272 seqs, 21671516995 residues
cleic sea	Septembe	US-10-79	1 agtaac	IDENTITY Gapop 10	3470272
OM nucleic - nuc	Run on:	Title: Perfect score:	Sequence:	Scoring table:	Searched:

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 80
Post-processing: Minimum Match 100\*
Listing first 150 summaries

1774092

Database : GenEmbl:\*

1: gb\_ba:\*
2: gb htg:\*
3: gb\_om:\*
4: gb\_om:\*
5: gb\_ov:\*
6: gb\_ov:\*
6: gb\_ov:\*
7: gb\_pat:\*
10: gb\_pat:\*
11: gb\_sts:\*
11: gb\_sts:\*
12: gb\_vi:\*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AR100077 Sequence	888	2531	198	AX816281 Sequence	AX074559 Sequence	671 Sequence	ADI/5616 Expressio	AJ521905 Arabidops	AX486274 Sequence	AX136053 Sequence	BD014871 Catalyst	AX484412 Sequence		AX008365 Sequence	BD218258 Newcastle	AR147539 Sequence	AR194187 Sequence	AR103699 Sequence	BD129929 Asthma-as	A35752 Synthetic o	0 Sequence	A35/51 Synthetic o AR168999 Semience	AR184398 Sequence	AX453001 Sequence	85 Mayet	6 Novel pla	55 2712 6 Semier	BD053979 Sequence	847006 D3S745 {VNT	AXZ41123 Sequence AX462717 Sequence	AJ531902 Arabidops	AS94// S.aureus pl AX165120 Sequence	E10288 Primer for		7 Sequence	2 Sequenc	3 Sequence		e Sequenci	] Sequence		7 Sequence	1 Sequence	7 Sequenci	sequence	o Sequenc	15459 Sequen
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0 139 11. 140 11. 141 11. 142 11. 143 11. 145 11. 147 11. 147 11. 147 11. 147 11. 0 148 11. 0 149 11. 0 150 11.	RESULT 1 AR100077 LOCUS DOCUS DEFINITION S ACCESSION P VERSION P VERYORDS SOURCE COGANISM I REFERENCE TITLE JOURNAL E FEATURES SOURCE OUTHORS TITLE AUTHORS TITLE AUTHORS TITLE BOUTOR	Query Match Best Local ( Matches 11 Qy 1	RESULT 2 AJ591807/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL
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Patent: WO 0026671-A 46 11-MAY-2000;
FRIEDRICHE ULRIKE (DE) ; CONNEX GMBH (DE) ; HEPPNER PETRA
RINGELS ACHIM (DE) ; LAKNER MERET (DE) ; CULLMANN GERHARD
REITER CHRISTIAN (DE)
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/organism="synthetic construct"

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|mol type="unassigned DNA"
|db_xref="taxon:32630"

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Sequence 46 from Patent WO0026671.
AX025318
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Sequence 54 from Patent WO0127612.
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PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante-info.infoblogen.fr).

Location/Qualifiers
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33 bp DNA linear PAT 17-JUL-2003
Novel method for detecting acid-resistant microorganisms in feces.
BD233882
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GOIN33/569,C07K16/12,G01N33/543,G01N33/577//C12P21/08,G01N33/
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1 (bases 1 to 33)
Relter, C., Cullmann, G., Friedrichs, U., Heppner, P., Lakner, M. and
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CHRISTIAN REITER,GERHARD CULLMANN,ULRIKE FRIEDRICHS,PETRA PI
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Coganism="Arabidopsis thaliana"
/mol type="Genomic DNA"
/culTivar="Wassillewskija"
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    .33
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bD241774.1 GI:33051544

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$ synthetic construct

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artificial sequences.

$ coreau, R. B. and Hefner, J. L.

Nucleic acids encoding taxus geranylgeranyl diphosphate synthase,

and methods of use

AL 10 2002529077-A 8 10-SEP-2002;

WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION

S Artificial Sequence

PN JP 2002529077-A/8

PD 10-SEP-2002

PR 05-NOV-1999 JP 2005881172

PR 05-NOV-1999 US 09/187050

PR 05-NOV-1999 US 09/187050

PC CI2N15/09, CI2NS/10, CI2N9/10, (CI2N19/10, CI2N1:91), CI2NI5/00, PC
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Patent: WO 0104324-A 3 18-JAN-2001;

INSTITUT MAIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;

INSTITUT NATIONAL DE LA SCHENCE APPLIQUEES DE TOULOUSE (FR) ;

Centre National De La Recherche Scientifique (FR)

Location/Qualifiers
                            BD241774 11-JUL-2003 Nucleic acids encoding taxus geranylgeranyl diphosphate synthase, and methods of use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium butyricum
Clostridium butyricum
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC Description of Artificial Sequence:PCR primer CC for synthesizing Tr295 truncation product FH Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sarcabal, P., Croux, C. and Soucaille, P. Method for preparing 1,3-propanediol by a recombinant micro-organism in the absence of coenzyme bl2 or one o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.0%; Score 13.6; DB 6; Length 28;
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/mol_type="unassigned DNA"
/db_xref="taxon:1492"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
69.0%; Score 13.8; DB 6;
Best Local Similarity 88.2%; Pred. No. 7.2e+04;
Matches 15; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AX074559 28 bp
Sequence 3 from Patent W00104324
AX074559 41:12710662
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Location/Qualifiers
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parent: EP 1336850-A 54 20-AUG-2003;
Connex Gesellschaft zur Optimierung von Forschung und Ent wicklung
                                                                                                                                                                                                                                                                                           Reiter, C., Cullmann, G., Heppner, P., Ringeis, A., Mueller, H. and Haindl, E.
Improved method for the detection of acid resistant microorganisms
                                                                                                                                                                                                                                                                                                                                                                               19-APR-2001;
Optimierung von Forschung und Entwicklung
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forganism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/note="CDR"

    .33
    ^organism="synthetic construct"
|mol_type="unassigned DNA"
|db_xref="taxon:32630"

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Sequence 54 from Patent EP1336850.
AX816281.
AX816281.1 GI:39646788
                                                                                                                          AX113614 33 bp
Sequence 54 from Patent WO0127613.
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Connex Gesellschaft zur
(DE)
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      AACATTAATGTTTGGTT 29
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Best Local Similarity
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Matches 15; Conserv
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Gaps

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PCR primer

PAT 06-FEB-2001

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS JOURNAL

TITLE

FEATURES

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PAT 29-SEP-1999
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Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATH521905 52 bp DNA linear PLN 29-MAR-2003
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lephiec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
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Ellis,N.A., German,J. and Groden,J.
Nucleic acids of the bloom's syndrome gene
Patent: US 5824501-A 14 20-0CT-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 13.2; DB 6;
Pred. No. 1.5e+05;
                                                                                                                                    Query Match 68.0%; Score 13.6; DB 6; Best Local Similarity 80.0%; Pred. No. 8.3e+04; Matches 16; Conservative 0; Mismatches 4;

    . 73
    forganism="synthetic construct"
|mol type="genomic DNA"
|db_xref="taxon:32630"

                                                                                                                                                                                                                                                                                                                                                 DNA
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Sequence 14 from patent US 5824501.
AR049025 AR049025.1 GI:6005064
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/wol_type="unassigned DNA"
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EMBO Rep. 3 (12), 1152-1157 (2002)
22363535
   Location/Qualifiers
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AJ521905
AJ521905.1 GI:26790141
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1 Similarity 83.3%;
15; Conservative
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Balzergue, S.
Direct Submission
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Best Local Similarity
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PC C12N15/09,C12N1/19,C12N9/16//(C12N1/19,C12R1:645),(C12N1/19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUL-2001 JP 2001222153
25-JUL-2000 DE 10036491.8
RAINER MUBLLER, JOHANN PETER THALHOFER, FRANK GEIPEL, WERNER
                       Gaps
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synthetic construct
synthetic construct
artificial sequences.

1 (bases 1 to 73)
Mueller,R. Thalhofer,J.P., Geipel,F., Hoelke,W., Glaser,S.,
Ekstein,H., Kirschbaum,T. and Riebel,B.B.N.
Expression of alkaline phosphatase in yeast
Patent:JP 2002253269-A 26 10-SEP-2002;
FHOFFMANN LA ROCHE AG
OS Artificial Sequence
PN JP 2002253269-A/26
                                                                                                                                                                                                                                                                                                                                                                Glaser, S.,
                                                                                                                                                                                                                                                                                                                                                             Mueller, R., Thalhofer, J.P., Geipel, F., Hoelke, W., Glaser, S. Eckstein, H., Kirschbaum, T. and Bommarius, B. Eckstesion of alkaline phosphatase in yeast Parent: EP 1176205-A 27 30-JAN-2002; Patent: EP 1176205-A 27 30-JAN-2002; Roche Diagnostics GmbH (DE); F. HOFFMANN-LA ROCHE AG (CH) Location/Qualifiers
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Description of Artificial Sequence: Artificial FH Key
Location/Qualifiers
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    .73
/organism='Artificial Sequence'.

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BD175616
Best Local Similarity 80.0%; Pred. No. 9.5e+04; Matches 16; Conservative ' 0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .73
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/noTe="Artificial"
                                                                                                                                                                                             DNA
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Sequence 27 from Patent EP1176205.
AX356671
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AX136051 34 bp
Sequence 3 from Patent EP1096014.
AX136051
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BD014871.1 GI:22555678
JP 2001161387-A/2.
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            the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-infobiogen.fr).
 plants from INRA (Versailles). The DNA fragment(s) resulting from
                                                                                                                                                                                              /mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="teaxon;3702"
/clone="280603"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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Candida albicans
Eukaryota; Pungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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Pred. No. 1.3e+05;
0; Mismatches 3;
                                                                                                                                                                                       /organism="Arabidopsis thaliana"
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/mol_type="unassigned DNA"
/db xref="taxon:5476"
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AX180638.1 GI:15132524
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1 (bases 1 to 34)
Chen,P., Kan,C.C., Luo,C., Margosiak,S., OGconnor,P., Russell,A.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAT 30-MAY-2001
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Tempczyk-Russel, A., Nguyen, B., Sarup, J.C., Gaur, S., Anderson, M.B.,
Dengy, Y.L., Lundgren, K. and Register, J.
Catalytic domain of the human effector cell cycle checkpoint
protein kinase, chkl, materials and methods for identification of
inhibitors thereof
Patent: EP 1096014-A 3 02-MAY-2001;
Agouron Pharmaceuticals, Inc. (US)
Agouron Cocation/Qualifiers
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State Admain of human effector cell cycle check point protein kinage Chkl, and substance for identifying the inhibitor and identification method.
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Osbourn, A.E., Haralampidis, K. and Bryan, G.T.
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="PCR primer"
                                                                                                                                                       /organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
/nofe="Primer"
                Plant gene
Patent: WO 0146391-A 216 28-JUN-2001;
Plant Bioscience Limited (GB)
Location/Qualifiers
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PAT 12-JUN-2003
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
Patent: WO 0138566A 475 31-MAY-2001;
Curagen Corporation (US)
                                                                                                                                                                                       1 (bases 1 to 47)
Cohen, D., Chumakov, I. and Blumenfeld, M.
Ballellic markers for use in constructing a high density disequilibrium map of the human genome
Patent: US 6537751-A 1887 25-MAR-2003;
Location/Qualifiers
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64.0%; Score 12.8; DB 6; Length 51;
Best Local Similarity 87.5%; Pred. No. 2.1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          Query Match
64.0%; Score 12.8; DB 6;
Best Local Similarity 87.5%; Pred. No. 2.1e+05;
Matches 14; Conservative 0; Mismatches 2;
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                                               AR290152 47 bp DN.
Sequence 1887 from patent US 6537751.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AX008365
AX008365.1 GI:9995921
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/organism="Homo sapiens"

    .47
    /organism="unknown"
    /mol_type="genomic DNA"

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Homo sapiens
                                                                                                                                                                          Unclassified.
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Nguyen, B., Sarup, J.C., Gaur, S., Anderson, M.B., Deng, Y.L., Lundgren, K. and Register, J. Catalyst domain of human effector cell cycle check point protein kinase Chkl, and substance for identifying the inhibitor and identification method

L. Patent: JP-2001161387-A 2 19-JUN-2001;
AGOURON PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2001161387-A/2
PD 19-JUN-2001
PF 01-NOV-2001
PF 01-NOV-2000
PR 01-NOV-2009 US 60/162887,14-DEC-1999 US 09/460421 PI
PING CHEN, CHEN CHEN KAN, CHUN LUO, STEVEN MARGOSIAK, PATRICK PI
                                                                                                                                                                                                                                       O'CONNOR,
PI ANNA TEMPCZYK RUSSELL, BINH NGUYEN, JAY CHAND SARUP, SMITA GAUR,
PI MARK BRIAN ANDERSON, YA LI DENG, KAREN LUNDGREN, JAMES REGISTER
PC CIZNIS/09, CO7K19/00, CIZNI/21, CIZNS/10, CIZNI/00, CIZN9/12, CIZN9/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Candida albicans
Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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(C12N5/00,C12R1:91)
Description of Artificial Sequence: PCR primer FH
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism='Artificial Sequence'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. 34
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Sequence 1712 from Patent W002053728.
AX484412
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/mol_type="unassigned DNA"
/db_xref="taxon:5476"
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AGTACCATCTATCTTT 22
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AX484412/c
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1 (bases 1 to 24)
O'DWYer,K.W. Warren,R. and Perry,C. Sec A2 from Streptococcus pneumoniae Patent: US 6204019-A 5 20-WAR-2001;
Location/Qualifiers
                                                                                             74 bp
Sequence 53 from patent US 6221597.
AR147539
AR147539.1 GI:15111342
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 5 from patent US 6348342.
AR194187.1 GI:20240779
                                                                                                                                                                                                                                                                                                                                                                              /mol_type="unassigned DNA"
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ARI42867.
ARI42867.1 GI:15104153
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/organism="unknown"
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50 AAATCTTTGTTTGGTT 35
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Roberts, C.J.
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Best Local Similarity 78.9
Matches 15; Conservative
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AR194187/c
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AR147539/c
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AR142867/c
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Patent: WO 9966045-A 17 23-DEC-1999;
BILLKENS ARNOUD LEONARD JOSEF (NL); KOCH GUUS (NL); LEEUW OLAV SVEN
DE (NL); PRETIERS BENNARDUS PETRUS HUBER (NL); STICHTING DIENST
LANDBOUWKUNDI (NL)
Location/Qualifiers
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Newcastle disease virus infectious clones, vaccines and diagnostic
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19-JUN-1998 EP 98202054.7
BERNARDUS PETRUS HUBERTUS PEETERS, OLAV SVEN
LEEUW, GUCH,
ARNOUD LEONARD JOSEF GIELKENS
C12N15/09,A61K39/17,A61K48/00,A61P31/12,C12N7/00,C12Q1/70, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                artificial sequences.
I (bases 1 to 5).
Peeters, B.P.H. Leeuw, O.S.D., Koch,G. and Gielkens,A.L.J.
Newcastle disease virus infectious clones, vaccines and diagnostic
                                                                       Gielkens, A.L., Koch, G., De Leeuw, O. and Peeters, B.P.
Newcastle disease virus infectious clones, vaccines and diagnostic
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OS Artificial Sequence
OS Artificial Sequence
PN JP 2002518012-A/17
PD 25-JUN-2002
PF 17-JUN-1999 JP 2000554854
PR 19-JUN-1999 BP 98202054.7
PI BERNARDUS PETRUS HUBERTUS PEETERS,OLAV SVEN
DE LEEUW,GUUS KOCH,
PI ARNOUD LEONARD JOSEF GIELKENS
PC C12N15/00
C12N15/00
CC /note='Primer BGL5F2'
CC Description of Artificial Sequence: primer
FH KEY
FT primer_bind (1). (58)
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Best Local Similarity 87.5%; Pred. No. 2e+05;

Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                64.0%; Score 12.8; DB 6; Length 58; 87.5%; Pred. No. 2e+05; Live 0; Mismatches 2; Indels
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Key

Location/Qualifiers

Location/Qualifiers
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/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
1. .58
/note="'Primer BGL5F2'
primer"
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JP 2002518012-A/17.
synthetic construct
synthetic construct
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Best Local Similarity 87.5
Matches 14; Conservative
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PAT 08-AUG-2001
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                                                                                                                                                                                    Essential genes of yeast as targets for antifungal agents, herbicides, insecticides and anti-proliferative drugs Patent: US 6221597-A 53 24-APR-2001; Location/Qualifiers
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Best Local Similarity 87.5%; Pred. No. 2e+05;
Matches 14; Conservative 0; Mismatches 2; Indels
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                    Topology: Linear;
Asthma-associated
         Strandedness: Single;
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Synthetic oligo 50.
A35752
A35752.1 GI:1927123
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artificial sequences.
1 (bases 1 to 35)
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I33654
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Brooks-Wilson,A.R., Buckler,A., Cardon,L., Carey,A.H., Galvin,M.,
Briller,A. and North,M.
Asthma related genes
Patent: US 6087485-A 223 11-JUL-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unidentified
unidentified
unidentified
unclassified.
E 1 (bases 1 to 27)
S Wilson,A.R.B., Buckler,A., Cardon,L., Carey,A.H., Galvin,M.,
Miller,A. and North,M.
Asthma-associated gene
L Patent: JP 2002500895-A 219 15-JAN-2002;
AXYS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002500895-A/219
PP 11-JAN-2002
PF 21-JAN-2002
PF 21-JAN-198 JP 200528715
PI ANGELA R BROOKS WILSON,ALAN BUCKLER,LON
CARDON,ALISOUN H CAREY,
PI MAKGARET GALVIN,ANDREW MILLER,MICHAEL NORTH
PC C12Q1/68,A01K67/027,CO7K14/47,C12N15/09,C12N15/00 CC
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                                                                                                                                  Score 12.6; DB 6; Length 24;
Pred. No. 2.9e+05;
0; Mismatches 4; Indels
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Pred. No. 2.8e+05;
0; Mismatches 4; Indels
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1 (bases 1 to 24)
O'Dwyer,K.M., Warren,R. and Perry,C. Compounds
Patent: US 6348342-A 5 19-FEB-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                           Sequence 223 from patent US 6087485. AR103699
                                                                1. .24
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="unassigned DNA"
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BD129929.1 GI:23224874
JP 2002500895-A/219.
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                                                                                                                              63.0%;
78.9%;
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Best Local Similarity 78.9%;
Matches 15; Conservative
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AR103699/c
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BD129929/c
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Patent: WO 9308273-A 50 29-APR-1993;
Location/Qualifiers
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                                                 /organism='Unidentified'. Location/Qualifiers
                                                                                                                                                                                                   Query Match
63.0%; Score 12.6; DB 6;
Best Local Similarity 78.9%; Pred. No. 2.8e+05;
Matches 15; Conservative 0; Mismatches 4;
               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 34)
Higaki,J.N., Tischer,E.G., Cordell,B. and
Production of homogeneous truncated CNTF
Patent: US 5593857-A 3 14-JAN-1997;
Location/Qualifiers
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/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
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/organism="unknown"
/wol_type="unassigned DNA"
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Sequence 3 from patent US 5593857.
133654
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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gene
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PAT 06-JUL-2002
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                                                                          Unclassified.

1 (bases 1 to 36)

1 (bases 1 to 36)

Ballance, D.J., Courtney, M.G., Finnis, C.J.A. and Sleep, D.

Modulation of cellular proliferation with thymidine phosphorylase Patent: US 6290953-A 49 18-SEP-2001;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki,Y.
method for base sequencing and biologically active nucleic acids
Patent: WO 0244195-A 15 06-JUN-2002;
RIKEN (JP)
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Stanley, C.John., Orum, H. and Jorgensen, M.
Nucleic acid analogs with a chelating functionality
Patent: US 6346378-A 11 12-FBB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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    .50
    /organism="synthetic construct"
/mol_type="unassigned DNA"

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/wol_type="unassigned DNA"

    .36
    /organism="unknown"
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AX453001
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AR168999
AR168999.1 GI:17906697
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synthetic construct
artificial sequences.
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Best Local Similarity 78.9
Matches 15; Conservative
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Best Local Similarity 7
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Unclassified.
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AR184398/c
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AX453001/c
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Unknown.
Unclassified.
1 (bases 1 to 35)
Ballance, D.J., Courtney, M.G., Finnis, C.J.A. and Sleep, D.
Ballance, D.J., Couttney, M.G., Finnis, C.J.A. and Sleep, D.
Modulation of cellular proliferation with thymidine phosphorylase
Patent: US 6290953-A 50 18-SEP-2001;
Location/Qualifiers
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63.0%; Score 12.6; DB 6; Length 36;
Best Local Similarity 78.9%; Pred. No. 2.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels
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 Score 12.6; DB 6; Length 35;
Pred. No. 2.7e+05;
0; Mismatches 4; Indels
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Pred. No. 2.7e+05;
0; Mismatches 4;

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|mol type="unassigned DNA"
|db_xref="taxon:32630"

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PATENT: WO 9308273-A 49 29-APR-1993;
Location/Qualifiers
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DEFINITION Sequence 49 from patent US 6290953.
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AR16000
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78.9%;
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Synthetic oligo 49.
A35751
A35751.1 GI:1927122
    Query Match
Best Local Similarity 78.9%;
Matches 15; Conservative (
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synthetic construct
artificial sequences.
1 (bases 1 to 36)
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Best Local Similarity 78.9 Matches 15; Conservative
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RESULT 31 A35751/c

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PAT 17-JUL-2003
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24-SEP-1999 JP 2000572337
25-SEP-1998 US 60/101939
MICHAEL W LASSNER, ROBIN A EMIG, DIANE M RUEZINSKY, ALISON VAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PC C12N15/09, A01H5/00, C12NS/10//C12N9/10, C12N15/00, C12N5/00 CC Description of Artificial Sequence: Synthetic Oligonucleotide FH Key
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Mayetiola destructor
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterrygota; Diptera; Nematocera; Sciaroidea;
1 (Dases I to 60)
Behura, S. K., Rider, S. D., Valicente, F. H. and Staurt, J. J.
Hessian fly STS markers
                                                                                                                                                                                                                                                                                                            DD22485.1 GI:33034596
JP 2002525105-A/175.
Synthetic construct
synthetic construct
artificial sequences.
I (bases I to 60)
Lassner, M. W., Emigy, R.A., Ruezinsky, D.M. and Eenennaam, A.V.
Novel plant acyltransferases
Patent: JP 2002525105-A 175 13-AUG-2002;
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    59
/note="polymorphic AFLP marker EAC/MCTG-82"

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        /map="between G15-1 and EAC/MCTA-201"
                                                                                 ch 63.0%; Score 12.6; DB 11;
1 Similarity 78.9%; Pred. No. 2.5e+05;
15; Conservative 0; Mismatches 4;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon.32630"
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BD224826
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JP 2002525105-A/175
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BV079655
BV079655.1 GI:34787404
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BV079655/c
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BD224826
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Submitted (27-SRP-2001) Entomology, Purdue University, 1158 Smith
Hall, West Lafayette, IN 47907-1158, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                        Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K.L. Gene disruption methodologies for drug target discovery Patent: WO 02053728-A 3059 11-JUL-2002; Elitra Pharmaceuticals, Inc. (US)
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                                                              63.0%; Score 12.6; DB 6; Length 50; 78.9%; Pred. No. 2.6e+05; ive 0; Mismatches 4; Indels
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/organism="Candida albicans"
/mol_type="unassigned DNA"
/db_xref="taxon:5476"
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/db_xref="taxon:39758"
/chromosome="X2"
/db_xref="taxon:32630"
/note="a spacer"
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Sequence 3069 from Patent
AX485769
                                                                                                                             1 AGTAACATCTATGTTTGGT 19
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Best Local Similarity 78.9
Matches 15; Conservative
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2 (bases 1 to 59)
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Matches 15; Conservative
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1 (bases 1 to 79)
Latif, F., Modi, W.S., Duh, F.M., Schmidt, L., Li, H., Geil, L., Modi, W.S., Duh, F.M., Schmidt, L., Li, H., Geil, L., Molecular and genetic characterization and physical mapping of 11 new markers detecting multiallele restriction fragment length polymorphisms on the short arm of human chromosome 3 Hum. Genet. 90 (1-2), 17-22 (1992)
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C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases I to 63) Edwards, J.B.D.M., Duclair, B. and Jordan, J.Y. Sequence tag and encoded human protein Patent: JP 2001269182-A 30225 02-OCT-2001;
                                                                                                                                                                                                            Hemo sapiens (human)
JP 2001269182-A/30225
02-OCT-2001
24-FEB-2000 JP 2000118773
25-FEB-1999 US 60/122487
JEAN BADUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
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Map location: 3p26.
Location/Qualifiers
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D38745 {VNTR repeat element} [human, Genomic, 79 nt].
S47006
S47006.1 GI:258800
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Pred. No. 2.5e+05;
0; Mismatches 4; Indels
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Sequence tag and encoded human protein.

    .79
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/db xref="taxon:9606"
1. 79
               BD053979
BD053979.1 GI:22599585
JP 2001269182-A/30225.
Homo sapiens (human)
Homo sapiens
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/gene="D3S745"
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1 Similarity 78.9%;
15; Conservative C
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PC C12P2
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Expressed sequence tags and encoded human proteins
Patent: EP 1033401-A 34309 06-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 12.6; DB 11; Length 60; Pred. No. 2.5e+05;
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Pred. No. 2.5e+05;
0; Mismatches 4; Indels
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                                                 Department of Entomology
Purdue University
901 W State St., West Lafayette, IN 47907, USA
Primer A: None provided
Primer B: None provided
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/db_xref="taxon:39758"
/clone lib="Hessian fly genomic DNA"
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'organism="Mayetiola destructor"
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    .63
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Total Vol:
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Best Local Similarity 78.9%;
Matches 15; Conservative
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Tris-Cl:
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                                   Contact: Jeff Stuart
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RESULT 42

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SOURCE

AUTHORS JOURNAL

FEATURES

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Malzert Submission

Microt Stands

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                                                                                                                                   ATH531902 37 bp DNA linear PLN 29-MAR-2003 Arabidopsis thaliana T-DNA flanking sequence, left border, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chavin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAMUPIRES 48 bp DNA linear BCT 02-MAR-1992 S.aureus plasmid DNA for part of mupirocin resistance gene (XhoI
                                                                                                                                                                                                                                                                      left border, T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 12.4; DB 8;
Pred. No. 3.4e+05;
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/note="T-DNA flanking sequence
left border"
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AJ531902.1 GI:26800162
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92.9%;
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Staphylococcus aureus
Staphylococcus aureus
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Balzergue, S.
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Best Local Similarity 92.9
Matches 13, Conservative
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X59477.1 GI:46621
20 CAGCTATGTTTGGT
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                                                                           RESULT 44
ATH531902
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JOURNAL
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KEYWORDS
SOURCE
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SAMUPIRES
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae,
Pooldeae, Triticeae, Aegilops.
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Microsatellite markers from Triticum tauschii
Patent: EP 121707-A 461 26-JUN-2002;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
Location/Qualifiers
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Gene disruption methodologies for drug target discovery
Patent: WO 0160975-A 361 23-AUG-2001;
Elitra Pharmaceuticals, Inc. (US)
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                                        Score 12.6; DB 9; Length 79;
Pred. No. 2.4e+05;
0; Mismatches 4; Indels
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Pred. No. 3.7e+05;
0; Mismatches 1; Indels
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Pred. No. 2.4e+05;
0; Mismatches 4;
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                           DNA
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/mol_type="unassigned DNA"
/db_xref="taxon:37682"
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Sequence 361 from Patent WO0160975.
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                                                                                                                                                       20
                                                                                                                                                                                                         3 Grada Agricitire 21
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                                     63.0%;
78.9%;
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78.9%;
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synthetic construct
artificial sequences.
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| Similarity 92.9%;
| 13; Conservative (
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                                     Query Match
Best Local Similarity
Matches 15; Conserv
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Matches 15; Conserv
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Best Local Similarity
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RESULT 43 AX462717/c LOCUS

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FEATURES

REFERENCE

KEYWORDS SOURCE

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TITLE
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Search completed: September 23, 2004, 16:21:00 Job time : 1274 secs

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